ANTISENSE MODULATION OF p38 MITOGEN ACTIVATED PROTEIN KINASE EXPRESSION

FIELD OF THE INVENTION

This invention relates to compositions and methods for modulating expression of p38 mitogen activated protein kinase genes, a family of naturally present cellular genes involved in signal transduction, and inflammatory and apoptotic responses. This invention is also directed to methods for inhibiting inflammation or apoptosis; these methods can be used diagnostically or therapeutically. Furthermore, this invention is directed to treatment of diseases or conditions associated with expression of p38 mitogen activated protein kinase genes.

BACKGROUND OF THE INVENTION

Cellular responses to external factors, such as growth factors, cytokines, and stress conditions, result in altered gene expression. These signals are transmitted from the cell surface to the nucleus by signal transduction pathways. Beginning with an external factor binding to an appropriate receptor, a cascade of signal transduction events is initiated. These responses are mediated through activation of various enzymes and the subsequent activation of specific transcription factors. These activated transcription factors then modulate the expression of specific genes.

The phosphorylation of enzymes plays a key role in the transduction of extracellular signals into the cell. Mitogen activated protein kinases (MAPKs), enzymes which effect such phosphorylations are targets for the action of growth factors, hormones, and other agents involved in cellular metabolism,

proliferation and differentiation (Cobb *et al., J. Biol. Chem.*, **1995**, *270*, 14843). Mitogen activated protein kinases were initially discovered due to their ability to be tyrosine phosphorylated in response to exposure to bacterial lipopolysaccharides or hyperosmotic conditons (Han *et al, Science*, **1994**, *265*, 808). These conditions activate inflammatory and apoptotic responses mediated by MAPK. In general, MAP kinases are involved in a variety of signal transduction pathways (sometimes overlapping and sometimes parallel) that function to convey extracellular stimuli to protooncogene products to modulate cellular proliferation and/or differentiation (Seger *et al., FASEB J.*, **1995**, *9*, 726; Cano *et al., Trends Biochem. Sci.*, **1995**, *20*, 117).

One of the MAPK signal transduction pathways involves the MAP kinases p38α and p38β(also known as CSaids Binding Proteins, CSBP). These MAP kinases are responsible for the phosphorylation of ATF-2, MEFC2 and a variety of other cellular effectors that may serve as substrates for p38 MAPK proteins (Kummer *et al, J. Biol. Chem.*, **1997**, *272*, 20490). Phosphorylation of p38 MAPKs potentiates the ability of these factors to activate transcription (Raingeaud *et al, Mol. Cell Bio.*, **1996**, *16*, 1247; Han et *al, Nature*, **1997**, *386*, 296). Among the genes activated by the p38 MAPK signaling pathway is IL-6 (De Cesaris, P., *et al., J. Biol. Chem.*, **1998**, *273*, 7566-7571).

Besides p38α and p38β, other p38 MAPK family members have been described, including p38γ (Li et *al, Biochem. Biophys. Res. Commun.*, **1996**, *228*, 334), and p38δ (Jiang *et al, J. Biol. Chem.*, **1997**, *272*, 30122). The term "p38" as used herein shall mean a member of the p38 MAPK family, including but not limited to p38α, p38β, p38γ and p38δ, their isoforms (Kumar *et al, Biochem. Biophys. Res. Commun.*, **1997**, *235*, 533)

and other members of the p38 MAPK family of proteins whether they function as p38 MAP kinases *per se* or not.

Modulation of the expression of one or more p38 MAPKs is desirable in order to interfere with inflammatory or apoptotic responses associated with disease states and to modulate the transcription of genes stimulated by ATF-2, MEFC2 and other p38 MAPK phosphorylation substrates.

Inhibitors of p38 MAPKs have been shown to have efficacy in animal models of arthritis (Badger, A.M., *et al.*, *J. Pharmacol. Exp. Ther.*, **1996**, *279*, 1453-1461) and angiogenesis (Jackson, J.R., *et al.*, *J. Pharmacol. Exp. Ther.*, **1998**, *284*, 687-692). MacKay, K. and Mochy-Rosen, D. (*J. Biol. Chem.*, **1999**, *274*, 6272-6279) demonstrate that an inhibitor of p38 MAPKs prevents apoptosis during ischemia in cardiac myocytes, suggesting that p38 MAPK inhibitors can be used for treating ischemic heart disease. p38 MAPK also is required for T-cell HIV-1 replication (Cohen *et al*, *Mol. Med.*, **1997**, *3*, 339) and may be a useful target for AIDS therapy. Other diseases believed to be amenable to treatment by inhibitors of p38 MAPKs are disclosed in US Patent No. 5,559,137, herein incorporated by reference.

Therapeutic agents designed to target p38 MAPKs include small molecule inhibitors and antisense oligonucleotides. Small molecule inhibitors based on pyridinyl imidazole are described in US Patent No. 5,670,527; 5,658,903; 5,656,644; 5,559,137; 5,593,992; and 5,593,991. WO 98/27098 and WO 99/00357 describe additional small molecule inhibitors, one of which has entered clinical trials. Other small molecule inhibitors are also known.

Antisense therapy represents a potentially more specific therapy for targeting p38 MAPKs and, in particular, specific p38 MAPK isoforms. Nagata, Y., *et al.* (*Blood*, **1998**, *6*, 1859-1869) disclose an antisense phosphothioester oligonucleotide targeted to the translational start site of mouse p38b (p38β).

Aoshiba, K., *et al.* (*J. Immunol.*, **1999**, *162*, 1692-1700) and Cohen, P.S., *et al.* (*Mol. Med.*, **1997**, *3*, 339-346) disclose a phosphorothioate antisense oligonucleotide targeted to the coding regions of human p38α, human p38β and rat p38.

There remains a long-felt need for improved compositions and methods for modulating the expression of p38 MAP kinases.

SUMMARY OF THE INVENTION

The present invention provides antisense compounds which are targeted to nucleic acids encoding a p38 MAPK and are capable of modulating p38 MAPK expression. The present invention also provides oligonucleotides targeted to nucleic acids encoding a p38 MAPK. The present invention also comprises methods of modulating the expression of a p38 MAPK, in cells and tissues, using the oligonucleotides of the invention. Methods of inhibiting p38 MAPK expression are provided; these methods are believed to be useful both therapeutically and diagnostically. These methods are also useful as tools, for example, for detecting and determining the role of p38 MAPKs in various cell functions and physiological processes and conditions and for diagnosing conditions associated with expression of p38 MAPKs.

The present invention also comprises methods for diagnosing and treating inflammatory diseases, particularly rheumatoid arthritis and asthma. These methods are believed to be useful, for example, in diagnosing p38 MAPK-associated disease progression. These methods employ the oligonucleotides of the invention. These methods are believed to be useful both therapeutically, including prophylactically, and as clinical research and diagnostic tools.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A-1B are graphs showing the effect of inhaled p38α MAP kinase antisense oligonucleotide ISIS 101757 (ASO, Fig. 1A) and mismatched control oligonucleotide ISIS 101758

(MM ASO, Fig. 1B) on ovalbumin (OVA)-induced airway hyperresponsiveness in a murine asthma model.

Figure 2 is a graph showing that inhaled ISIS 101757 increases the provocation concentration of methacholine required to achieve doubling of airway reactivity (PC200) in OVA-challenged mice.

Figures 3A-3B are graphs showing the effect of inhaled ISIS 101757 (Fig. 3A) and 101758 (Fig. 3B) on immune cells in broncheolar lavage (BAL) fluid of OVA-challenged mice. EOS=eosinpophils, NEU=neutrophils, MAC=macrophages, LYM=lymphocyes.

Figure 4 is a graph showing aerosolized ISIS 101757 concentration in mouse lung vs. dose.

Figure 5 is a graph showing dose-dependent inhibition of the penh response to methacholine (50 mg/ml) challenge by ISIS 101757. ISIS 101757 doses are in mg/kg (x-axis).

Figure 6 is a graph showing ISIS 101757 concentration (μg/g) in the lungs vs. dose (intratracheal administration).

DETAILED DESCRIPTION OF THE INVENTION

p38 MAPKs play an important role in signal transduction in response to cytokines, growth factors and other cellular stimuli. Specific responses elicited by p38 include inflammatory and apoptotic responses. Modulation of p38 may be useful in the treatment of inflammatory diseases, such as rheumatoid arthritis.

The present invention employs antisense compounds, particularly oligonucleotides, for use in modulating the function of nucleic acid molecules encoding a p38 MAPK, ultimately modulating the amount of a p38 MAPK produced. This is accomplished by providing oligonucleotides which specifically hybridize with nucleic acids, preferably mRNA, encoding a p38 MAPK.

The antisense compounds may be used to modulate the function of a particular p38 MAPK isoform, e.g. for research purposes to determine the role of a particular isoform in a normal or disease process, or to treat a disease or condition that may be associated with a particular isoform. It may also be desirable to target multiple p38 MAPK isoforms. In each case, antisense compounds can be designed by taking advantage of sequence homology between the various isoforms. If an antisense compound to a particular isoform is desired, then the antisense compound is designed to a unique region in the desired isoform's gene sequence. With such a compound, it is desirable that this compound does not inhibit the expression of other isoforms. Less desirable, but acceptable, are compounds that do not "substantially" inhibit other isoforms. By "substantially", it is intended that these compounds do not inhibit the expression of other isoforms by more than 10%, preferably not by more than 25%. If an antisense compound is desired to target multiple p38 isoforms, then regions of significant homology between the isoforms can be used.

This relationship between an antisense compound such as an oligonucleotide and its complementary nucleic acid target, to which it hybridizes, is commonly referred to as "antisense". "Targeting" an oligonucleotide to a chosen nucleic acid target, in the context of this invention, is a multistep process. The process usually begins with identifying a nucleic acid sequence whose function is to be modulated. This may be, as examples, a cellular gene (or mRNA made from the gene) whose expression is associated with a particular disease state, or a foreign nucleic acid from an infectious agent. In the present invention, the target is a nucleic acid encoding a p38 MAPK; in other words, a p38 MAPK gene or RNA expressed from a p38 MAPK gene. p38 MAPK mRNA is presently the preferred target. The targeting process also includes determination of a site or sites within the nucleic

acid sequence for the antisense interaction to occur such that modulation of gene expression will result.

In accordance with this invention, persons of ordinary skill in the art will understand that messenger RNA includes not only the information to encode a protein using the three letter genetic code, but also associated ribonucleotides which form a region known to such persons as the 5'-untranslated region, the 3'-untranslated region, the 5' cap region and intron/exon junction ribonucleotides. Thus, oligonucleotides may be formulated in accordance with this invention which are targeted wholly or in part to these associated ribonucleotides as well as to the informational ribonucleotides. The oligonucleotide may therefore be specifically hybridizable with a transcription initiation site region, a translation initiation codon region, a 5' cap region, an intron/exon junction, coding sequences, a translation termination codon region or sequences in the 5'- or 3'-untranslated region. Since, as is known in the art, the translation initiation codon is typically 5'-AUG (in transcribed mRNA molecules; 5'-ATG in the corresponding DNA molecule), the translation initiation codon is also referred to as the "AUG codon," the "start codon" or the "AUG start codon." A minority of genes have a translation initiation codon having the RNA sequence 5'-GUG, 5'-UUG or 5'-CUG, and 5'-AUA, 5'-ACG and 5'-CUG have been shown to function *in vivo*. Thus, the terms "translation initiation codon" and "start codon" can encompass many codon sequences, even though the initiator amino acid in each instance is typically methionine (in eukaryotes) or formylmethionine (prokaryotes). It is also known in the art that eukaryotic and prokaryotic genes may have two or more alternative start codons, any one of which may be preferentially utilized for translation initiation in a particular cell type or tissue, or under a particular set of conditions. In the context of the invention, "start codon" and "translation initiation codon" refer to the codon or

codons that are used *in vivo* to initiate translation of an mRNA molecule transcribed from a gene encoding p38, regardless of the sequence(s) of such codons. It is also known in the art that a translation termination codon (or "stop codon") of a gene may have one of three sequences, i.e., 5'-UAA, 5'-UAG and 5'-UGA (the corresponding DNA sequences are 5'-TAA, 5'-TAG and 5'-TGA, respectively). The terms "start codon region" and "translation initiation codon region" refer to a portion of such an mRNA or gene that encompasses from about 25 to about 50 contiguous nucleotides in either direction (i.e., 5' or 3') from a translation initiation codon. This region is a preferred target region. Similarly, the terms "stop codon region" and "translation termination codon region" refer to a portion of such an mRNA or gene that encompasses from about 25 to about 50 contiguous nucleotides in either direction (i.e., 5' or 3') from a translation termination codon. This region is a preferred target region. The open reading frame (ORF) or "coding region," which is known in the art to refer to the region between the translation initiation codon and the translation termination codon, is also a region which may be targeted effectively. Other preferred target regions include the 5' untranslated region (5'UTR), known in the art to refer to the portion of an mRNA in the 5' direction from the translation initiation codon, and thus including nucleotides between the 5' cap site and the translation initiation codon of an mRNA or corresponding nucleotides on the gene) and the 3' untranslated region (3'UTR), known in the art to refer to the portion of an mRNA in the 3' direction from the translation termination codon, and thus including nucleotides between the translation termination codon and 3' end of an mRNA or corresponding nucleotides on the gene). mRNA splice sites may also be preferred target regions, and are particularly useful in situations where aberrant splicing is implicated in disease, or where an overproduction of a particular mRNA splice product is implicated in disease.

Aberrant fusion junctions due to rearrangements or deletions may also be preferred targets.

Once the target site or sites have been identified, oligonucleotides are chosen which are sufficiently complementary to the target, i.e., hybridize sufficiently well and with sufficient specificity, to give the desired modulation.

"Hybridization", in the context of this invention, means hydrogen bonding, also known as Watson-Crick base pairing, between complementary bases, usually on opposite nucleic acid strands or two regions of a nucleic acid strand. Guanine and cytosine are examples of complementary bases which are known to form three hydrogen bonds between them. Adenine and thymine are examples of complementary bases which form two hydrogen bonds between them.

"Specifically hybridizable" and "complementary" are terms which are used to indicate a sufficient degree of complementarity such that stable and specific binding occurs between the DNA or RNA target and the oligonucleotide.

It is understood that an oligonucleotide need not be 100% complementary to its target nucleic acid sequence to be specifically hybridizable. An oligonucleotide is specifically hybridizable when binding of the oligonucleotide to the target interferes with the normal function of the target molecule to cause a loss of utility, and there is a sufficient degree of complementarity to avoid non-specific binding of the oligonucleotide to non-target sequences under conditions in which specific binding is desired, i.e., under physiological conditions in the case of *in vivo* assays or therapeutic treatment and, in the case of *in vitro* assays, under conditions in which the assays are conducted.

Hybridization of antisense oligonucleotides with mRNA interferes with one or more of the normal functions of mRNA. The functions of mRNA to be interfered with include all vital functions such as, for example, translocation of the RNA to

the site of protein translation, translation of protein from the RNA, splicing of the RNA to yield one or more mRNA species, and catalytic activity which may be engaged in by the RNA.

The overall effect of interference with mRNA function is modulation of p38 MAPK expression. In the context of this invention "modulation" means either inhibition or stimulation; i.e., either a decrease or increase in expression. In one embodiment, p38 MAPK expression is inhibited by at least 10%, by at least 20%, by at least 30%, by at least 40% and preferably by at least 50%.

Modulation of target (i.e., p38 MAPK) expression can be measured in ways which are routine in the art, for example by Northern blot assay of mRNA expression as taught in the examples of the instant application or by Western blot or ELISA assay of protein expression, or by an immunoprecipitation assay of protein expression, as taught in the examples of the instant application. Effects on cell proliferation or tumor cell growth can also be measured, as taught in the examples of the instant application.

The oligonucleotides of this invention can be used in diagnostics, therapeutics, prophylaxis, and as research reagents and in kits. Since the oligonucleotides of this invention hybridize to nucleic acids encoding a p38 MAPK, sandwich, colorimetric and other assays can easily be constructed to exploit this fact. Furthermore, since the oligonucleotides of this invention hybridize specifically to nucleic acids encoding particular isoforms of p38 MAPK, such assays can be devised for screening of cells and tissues for particular p38 MAPK isoforms. Such assays can be utilized for diagnosis of diseases associated with various p38 MAPK isoforms. Provision of means for detecting hybridization of oligonucleotide with a p38 MAPK gene or mRNA can routinely be accomplished. Such provision may include enzyme conjugation, radiolabelling or any other suitable detection systems. Kits

for detecting the presence or absence of p38 MAPK may also be prepared.

The present invention is also suitable for diagnosing abnormal inflammatory states in tissue or other samples from patients suspected of having an inflammatory disease such as rheumatoid arthritis. The ability of the oligonucleotides of the present invention to inhibit inflammation may be employed to diagnose such states. A number of assays may be formulated employing the present invention, which assays will commonly comprise contacting a tissue sample with an oligonucleotide of the invention under conditions selected to permit detection and, usually, quantitation of such inhibition. In the context of this invention, to "contact" tissues or cells with an oligonucleotide or oligonucleotides means to add the oligonucleotide(s), usually in a liquid carrier, to a cell suspension or tissue sample, either *in vitro* or *ex vivo*, or to administer the oligonucleotide(s) to cells or tissues within an animal. Similarly, the present invention can be used to distinguish p38 MAPK-associated diseases, from diseases having other etiologies, in order that an efficacious treatment regime can be designed.

The oligonucleotides of this invention may also be used for research purposes. Thus, the specific hybridization exhibited by the oligonucleotides may be used for assays, purifications, cellular product preparations and in other methodologies which may be appreciated by persons of ordinary skill in the art.

In the context of this invention, the term "oligonucleotide" refers to an oligomer or polymer of ribonucleic acid or deoxyribonucleic acid. This term includes oligonucleotides composed of naturally-occurring nucleobases, sugars and covalent intersugar (backbone) linkages as well as oligonucleotides having non-naturally-occurring portions which function similarly. Such modified or substituted oligonucleotides are often preferred over native forms because

of desirable properties such as, for example, enhanced cellular uptake, enhanced binding to target and increased stability in the presence of nucleases.

The antisense compounds in accordance with this invention preferably comprise from about 5 to about 50 nucleobases. Particularly preferred are antisense oligonucleotides comprising from about 8 to about 30 nucleobases (i.e. from about 8 to about 30 linked nucleosides), from about 20 to about 50 nucleobases, from about 20 to about 30 nucleobases, from about 13 to about 30 nucleobases, or from about 19 to about 23 nucleobases. Preferred embodiments comprise at least an 8-nucleobase portion of a sequence of an antisense compound which inhibits the expression of a p38 mitogen activated kinase. As is known in the art, a nucleoside is a base-sugar combination. The base portion of the nucleoside is normally a heterocyclic base. The two most common classes of such heterocyclic bases are the purines and the pyrimidines. Nucleotides are nucleosides that further include a phosphate group covalently linked to the sugar portion of the nucleoside. For those nucleosides that include a pentofuranosyl sugar, the phosphate group can be linked to either the 2', 3' or 5' hydroxyl moiety of the sugar. In forming oligonucleotides, the phosphate groups covalently link adjacent nucleosides to one another to form a linear polymeric compound. In turn the respective ends of this linear polymeric structure can be further joined to form a circular structure, however, open linear structures are generally preferred. Within the oligonucleotide structure, the phosphate groups are commonly referred to as forming the internucleoside backbone of the oligonucleotide. The normal linkage or backbone of RNA and DNA is a 3' to 5' phosphodiester linkage.

While the preferred form of antisense compound is a single-stranded antisense oligonucleotide, in many species the introduction of double-stranded structures, such as double-

stranded RNA (dsRNA) molecules, has been shown to induce potent and specific antisense-mediated reduction of the function of a gene or its associated gene products. This phenomenon occurs in both plants and animals and is believed to have an evolutionary connection to viral defense and transposon silencing.

The first evidence that dsRNA could lead to gene silencing in animals came in 1995 from work in the nematode, *Caenorhabditis elegans* (Guo and Kempheus, *Cell*, **1995**, 81, 611-620). Montgomery et al. have shown that the primary interference effects of dsRNA are posttranscriptional (Montgomery et al., *Proc. Natl. Acad. Sci. USA*, **1998**, *95*, 15502-15507). The posttranscriptional antisense mechanism defined in *Caenorhabditis elegans* resulting from exposure to double-stranded RNA (dsRNA) has since been designated RNA interference (RNAi). This term has been generalized to mean antisense-mediated gene silencing involving the introduction of dsRNA leading to the sequence-specific reduction of endogenous targeted mRNA levels (Fire et al., *Nature*, **1998**, 391, 806-811). Recently, it has been shown that it is, in fact, the single-stranded RNA oligomers of antisense polarity of the dsRNAs which are the potent inducers of RNAi (Tijsterman et al., *Science*, **2002**, *295*, 694-697). Single stranded and double stranded RNA (RNAi) inhibition of human p38 MAP kinase is also within the scope of the present invention.

Oligomer and Monomer Modifications

As is known in the art, a nucleoside is a base-sugar combination. The base portion of the nucleoside is normally a heterocyclic base. The two most common classes of such heterocyclic bases are the purines and the pyrimidines. Nucleotides are nucleosides that further include a phosphate group covalently linked to the sugar portion of the

nucleoside. For those nucleosides that include a pentofuranosyl sugar, the phosphate group can be linked to either the 2', 3' or 5' hydroxyl moiety of the sugar. In forming oligonucleotides, the phosphate groups covalently link adjacent nucleosides to one another to form a linear polymeric compound. In turn, the respective ends of this linear polymeric compound can be further joined to form a circular compound, however, linear compounds are generally preferred. In addition, linear compounds may have internal nucleobase complementarity and may therefore fold in a manner as to produce a fully or partially double-stranded compound. Within oligonucleotides, the phosphate groups are commonly referred to as forming the internucleoside linkage or in conjunction with the sugar ring the backbone of the oligonucleotide. The normal internucleoside linkage that makes up the backbone of RNA and DNA is a 3' to 5' phosphodiester linkage.

Modified Internucleoside Linkages

Specific examples of preferred antisense oligomeric compounds useful in this invention include oligonucleotides containing modified e.g. non-naturally occurring internucleoside linkages. As defined in this specification, oligonucleotides having modified internucleoside linkages include internucleoside linkages that retain a phosphorus atom and internucleoside linkages that do not have a phosphorus atom. For the purposes of this specification, and as sometimes referenced in the art, modified oligonucleotides that do not have a phosphorus atom in their internucleoside backbone can also be considered to be oligonucleosides.

In the *C. elegans* system, modification of the internucleotide linkage (phosphorothioate) did not significantly interfere with RNAi activity. Based on this observation, it is suggested that certain preferred oligomeric compounds of the invention can also have one or more modified

internucleoside linkages. A preferred phosphorus containing modified internucleoside linkage is the phosphorothioate internucleoside linkage.

Preferred modified oligonucleotide backbones containing a phosphorus atom therein include, for example, phosphorothioates, chiral phosphorothioates, phosphorodithioates, phosphotriesters, aminoalkylphosphotriesters, methyl and other alkyl phosphonates including 3'-alkylene phosphonates, 5'-alkylene phosphonates and chiral phosphonates, phosphinates, phosphoramidates including 3'-amino phosphoramidate and aminoalkylphosphoramidates, thionophosphoramidates, thionoalkylphosphonates, thionoalkylphosphotriesters, selenophosphates and boranophosphates having normal 3'-5' linkages, 2'-5' linked analogs of these, and those having inverted polarity wherein one or more internucleotide linkages is a 3' to 3', 5' to 5' or 2' to 2' linkage. Preferred oligonucleotides having inverted polarity comprise a single 3' to 3' linkage at the 3'-most internucleotide linkage i.e. a single inverted nucleoside residue which may be abasic (the nucleobase is missing or has a hydroxyl group in place thereof). Various salts, mixed salts and free acid forms are also included.

Representative United States patents that teach the preparation of the above phosphorus-containing linkages include, but are not limited to, U.S.: 3,687,808; 4,469,863; 4,476,301; 5,023,243; 5,177,196; 5,188,897; 5,264,423; 5,276,019; 5,278,302; 5,286,717; 5,321,131; 5,399,676; 5,405,939; 5,453,496; 5,455,233; 5,466,677; 5,476,925; 5,519,126; 5,536,821; 5,541,306; 5,550,111; 5,563,253; 5,571,799; 5,587,361; 5,194,599; 5,565,555; 5,527,899; 5,721,218; 5,672,697 and 5,625,050, certain of which are commonly owned with this application, and each of which is herein incorporated by reference.

In more preferred embodiments of the invention, oligomeric compounds have one or more phosphorothioate and/or

heteroatom internucleoside linkages, in particular $-CH_2-NH-O-CH_2-$, $-CH_2-N(CH_3)-O-CH_2-$ [known as a methylene (methylimino) or MMI backbone], $-CH_2-O-N(CH_3)-CH_2-$, $-CH_2-N(CH_3)-N(CH_3)-CH_2-$ and $-O-N(CH_3)-CH_2-CH_2-$ [wherein the native phosphodiester internucleotide linkage is represented as $-O-P(=O)(OH)-O-CH_2-$]. The MMI type internucleoside linkages are disclosed in the above referenced U.S. patent 5,489,677. Preferred amide internucleoside linkages are disclosed in the above referenced U.S. patent 5,602,240.

Preferred modified oligonucleotide backbones that do not include a phosphorus atom therein have backbones that are formed by short chain alkyl or cycloalkyl internucleoside linkages, mixed heteroatom and alkyl or cycloalkyl internucleoside linkages, or one or more short chain heteroatomic or heterocyclic internucleoside linkages. These include those having morpholino linkages (formed in part from the sugar portion of a nucleoside); siloxane backbones; sulfide, sulfoxide and sulfone backbones; formacetyl and thioformacetyl backbones; methylene formacetyl and thioformacetyl backbones; riboacetyl backbones; alkene containing backbones; sulfamate backbones; methyleneimino and methylenehydrazino backbones; sulfonate and sulfonamide backbones; amide backbones; and others having mixed N, O, S and CH_2 component parts.

Representative United States patents that teach the preparation of the above oligonucleosides include, but are not limited to, U.S.: 5,034,506; 5,166,315; 5,185,444; 5,214,134; 5,216,141; 5,235,033; 5,264,562; 5,264,564; 5,405,938; 5,434,257; 5,466,677; 5,470,967; 5,489,677; 5,541,307; 5,561,225; 5,596,086; 5,602,240; 5,610,289; 5,602,240; 5,608,046; 5,610,289; 5,618,704; 5,623,070; 5,663,312; 5,633,360; 5,677,437; 5,792,608; 5,646,269 and 5,677,439, certain of which are commonly owned with this application, and each of which is herein incorporated by reference.

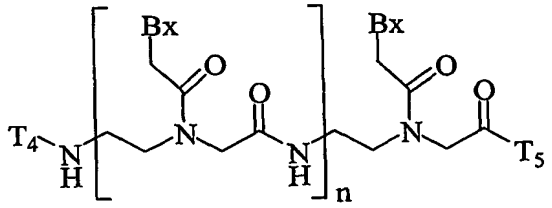
Oligomer Mimetics

Another preferred group of oligomeric compounds amenable to the present invention includes oligonucleotide mimetics. The term mimetic as it is applied to oligonucleotides is intended to include oligomeric compounds wherein only the furanose ring or both the furanose ring and the internucleotide linkage are replaced with novel groups, replacement of only the furanose ring is also referred to in the art as being a sugar surrogate. The heterocyclic base moiety or a modified heterocyclic base moiety is maintained for hybridization with an appropriate target nucleic acid. One such oligomeric compound, an oligonucleotide mimetic that has been shown to have excellent hybridization properties, is referred to as a peptide nucleic acid (PNA). In PNA oligomeric compounds, the sugar-backbone of an oligonucleotide is replaced with an amide containing backbone, in particular an aminoethylglycine backbone. The nucleobases are retained and are bound directly or indirectly to aza nitrogen atoms of the amide portion of the backbone. Representative United States patents that teach the preparation of PNA oligomeric compounds include, but are not limited to, U.S.: 5,539,082; 5,714,331; and 5,719,262, each of which is herein incorporated by reference. Further teaching of PNA oligomeric compounds can be found in Nielsen *et al.*, *Science*, **1991**, 254, 1497-1500.

One oligonucleotide mimetic that has been reported to have excellent hybridization properties is peptide nucleic acids (PNA). The backbone in PNA compounds is two or more linked aminoethylglycine units which gives PNA an amide containing backbone. The heterocyclic base moieties are bound directly or indirectly to aza nitrogen atoms of the amide portion of the backbone. Representative United States patents that teach the preparation of PNA compounds include, but are not limited to, U.S.: 5,539,082; 5,714,331; and 5,719,262, each of which is herein incorporated by reference. Further

teaching of PNA compounds can be found in Nielsen et al., Science, 1991, 254, 1497-1500.

PNA has been modified to incorporate numerous modifications since the basic PNA structure was first prepared. The basic structure is shown below:



wherein

Bx is a heterocyclic base moiety;

T_4 is hydrogen, an amino protecting group, $-C(O)R_5$, substituted or unsubstituted C_1-C_{10} alkyl, substituted or unsubstituted C_2-C_{10} alkenyl, substituted or unsubstituted C_2-C_{10} alkynyl, alkylsulfonyl, arylsulfonyl, a chemical functional group, a reporter group, a conjugate group, a D or L α-amino acid linked via the α-carboxyl group or optionally through the ω-carboxyl group when the amino acid is aspartic acid or glutamic acid or a peptide derived from D, L or mixed D and L amino acids linked through a carboxyl group, wherein the substituent groups are selected from hydroxyl, amino, alkoxy, carboxy, benzyl, phenyl, nitro, thiol, thioalkoxy, halogen, alkyl, aryl, alkenyl and alkynyl;

T_5 is $-OH$, $-N(Z_1)Z_2$, R_5, D or L α-amino acid linked via the α-amino group or optionally through the ω-amino group when the amino acid is lysine or ornithine or a peptide derived from D, L or mixed D and L amino acids linked through an amino group, a chemical functional group, a reporter group or a conjugate group;

Z_1 is hydrogen, C_1-C_6 alkyl, or an amino protecting group;

Z_2 is hydrogen, C_1-C_6 alkyl, an amino protecting group, $-C(=O)-(CH_2)_n-J-Z_3$, a D or L α-amino acid linked via the α-carboxyl group or optionally through the ω-carboxyl group when

the amino acid is aspartic acid or glutamic acid or a peptide derived from D, L or mixed D and L amino acids linked through a carboxyl group;

Z_3 is hydrogen, an amino protecting group, $-C_1-C_6$ alkyl, $-C(=O)-CH_3$, benzyl, benzoyl, or $-(CH_2)_n-N(H)Z_1$;

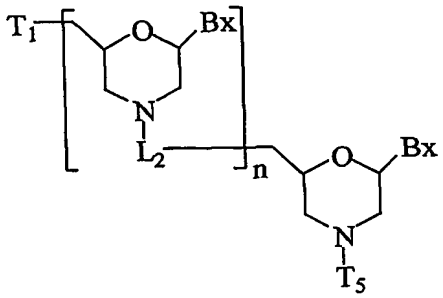
each J is O, S or NH;

R_5 is a carbonyl protecting group; and

n is from 2 to about 50.

Another class of oligonucleotide mimetic that has been studied is based on linked morpholino units (morpholino nucleic acid) having heterocyclic bases attached to the morpholino ring. A number of linking groups have been reported that link the morpholino monomeric units in a morpholino nucleic acid. A preferred class of linking groups have been selected to give a non-ionic oligomeric compound. The non-ionic morpholino-based oligomeric compounds are less likely to have undesired interactions with cellular proteins. Morpholino-based oligomeric compounds are non-ionic mimics of oligonucleotides which are less likely to form undesired interactions with cellular proteins (Dwaine A. Braasch and David R. Corey, *Biochemistry*, **2002**, *41(14)*, 4503-4510). Morpholino-based oligomeric compounds are disclosed in United States Patent 5,034,506, issued July 23, 1991. The morpholino class of oligomeric compounds have been prepared having a variety of different linking groups joining the monomeric subunits.

Morpholino nucleic acids have been prepared having a variety of different linking groups (L_2) joining the monomeric subunits. The basic formula is shown below:



wherein

T_1 is hydroxyl or a protected hydroxyl;

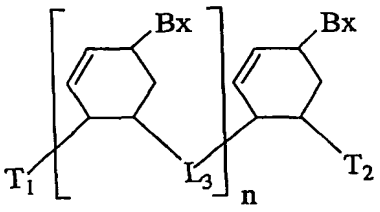
T_5 is hydrogen or a phosphate or phosphate derivative;

L_2 is a linking group; and

n is from 2 to about 50.

A further class of oligonucleotide mimetic is referred to as cyclohexenyl nucleic acids (CeNA). The furanose ring normally present in an DNA/RNA molecule is replaced with a cyclohenyl ring. CeNA DMT protected phosphoramidite monomers have been prepared and used for oligomeric compound synthesis following classical phosphoramidite chemistry. Fully modified CeNA oligomeric compounds and oligonucleotides having specific positions modified with CeNA have been prepared and studied (see Wang *et al.*, *J. Am. Chem. Soc.*, **2000**, *122*, 8595-8602). In general the incorporation of CeNA monomers into a DNA chain increases its stability of a DNA/RNA hybrid. CeNA oligoadenylates formed complexes with RNA and DNA complements with similar stability to the native complexes. The study of incorporating CeNA structures into natural nucleic acid structures was shown by NMR and circular dichroism to proceed with easy conformational adaptation. Furthermore the incorporation of CeNA into a sequence targeting RNA was stable to serum and able to activate E. Coli RNase resulting in cleavage of the target RNA strand.

The general formula of CeNA is shown below:



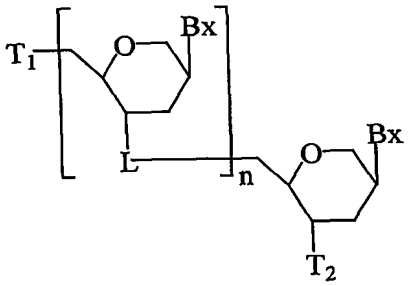
wherein

each Bx is a heterocyclic base moiety;

T_1 is hydroxyl or a protected hydroxyl; and

T2 is hydroxyl or a protected hydroxyl.

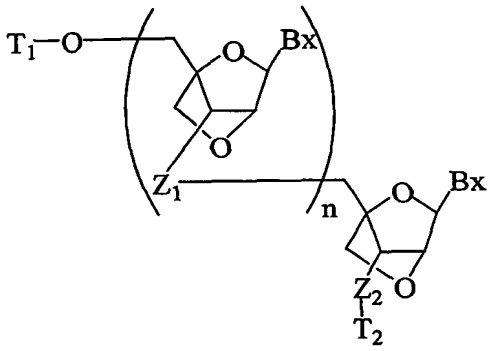
Another class of oligonucleotide mimetic (anhydrohexitol nucleic acid) can be prepared from one or more anhydrohexitol nucleosides (see, Wouters and Herdewijn, *Bioorg. Med. Chem. Lett.*, **1999**, *9*, 1563-1566) and would have the general formula:



A further preferred modification includes Locked Nucleic Acids (LNAs) in which the 2'-hydroxyl group is linked to the 4' carbon atom of the sugar ring thereby forming a 2'-C,4'-C-oxymethylene linkage thereby forming a bicyclic sugar moiety. The linkage is preferably a methylene $(-CH_2-)_n$ group bridging the 2' oxygen atom and the 4' carbon atom wherein n is 1 or 2 (Singh et al., Chem. Commun., 1998, 4, 455-456). When n is 1 (i.e, a methylene group) the modification is commonly referred to as LNA, and where n is 2 (i.e., an ethylene group) the modification is commonly referred to as ENA, which is a form of LNA. LNA and LNA analogs display very high duplex thermal

stabilities with complementary DNA and RNA (Tm = +3 to +10 C), stability towards 3'-exonucleolytic degradation and good solubility

properties. The basic structure of LNA showing the bicyclic ring system is shown below:



The conformations of LNAs determined by 2D NMR spectroscopy have shown that the locked orientation of the LNA nucleotides, both in single-stranded LNA and in duplexes, constrains the phosphate backbone in such a way as to introduce a higher population of the N-type conformation (Petersen et al., J. Mol. Recognit., 2000, 13, 44-53). These conformations are associated with improved stacking of the nucleobases (Wengel et al., Nucleosides Nucleotides, 1999, 18, 1365-1370).

LNA has been shown to form exceedingly stable LNA:LNA duplexes (Koshkin et al., J. Am. Chem. Soc., 1998, 120, 13252-13253). LNA:LNA hybridization was shown to be the most thermally stable nucleic acid type duplex system, and the RNA-mimicking character of LNA was established at the duplex level. Introduction of 3 LNA monomers (T or A) significantly increased melting points (Tm = +15/+11) toward DNA complements. The universality of LNA-mediated hybridization has been stressed by the formation of exceedingly stable LNA:LNA duplexes. The RNA-mimicking of LNA was reflected with

regard to the N-type conformational restriction of the monomers and to the secondary structure of the LNA:RNA duplex.

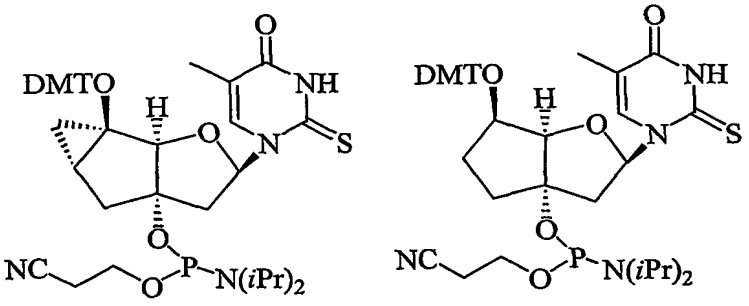
LNAs also form duplexes with complementary DNA, RNA or LNA with high thermal affinities. Circular dichroism (CD) spectra show that duplexes involving fully modified LNA (esp. LNA:RNA) structurally resemble an A-form RNA:RNA duplex. Nuclear magnetic resonance (NMR) examination of an LNA:DNA duplex confirmed the 3'-endo conformation of an LNA monomer. Recognition of double-stranded DNA has also been demonstrated suggesting strand invasion by LNA. Studies of mismatched sequences show that LNAs obey the Watson-Crick base pairing rules with generally improved selectivity compared to the corresponding unmodified reference strands.

Novel types of LNA-oligomeric compounds, as well as the LNAs, are useful in a wide range of diagnostic and therapeutic applications. Among these are antisense applications, PCR applications, strand-displacement oligomers, substrates for nucleic acid polymerases and generally as nucleotide based drugs. Potent and nontoxic antisense oligonucleotides containing LNAs have been described (Wahlestedt et al., Proc. Natl. Acad. Sci. U. S. A., 2000, 97, 5633-5638.) The authors have demonstrated that LNAs confer several desired properties to antisense agents. LNA/DNA copolymers were not degraded readily in blood serum and cell extracts. LNA/DNA copolymers exhibited potent antisense activity in assay systems as disparate as G-protein-coupled receptor signaling in living rat brain and detection of reporter genes in Escherichia coli. Lipofectin-mediated efficient delivery of LNA into living human breast cancer cells has also been accomplished.

The synthesis and preparation of the LNA monomers adenine, cytosine, guanine, 5-methyl-cytosine, thymine and uracil, along with their oligomerization, and nucleic acid recognition properties have been described (Koshkin et al., Tetrahedron, 1998, 54, 3607-3630). LNAs and preparation thereof are also described in WO 98/39352 and WO 99/14226.

The first analogs of LNA, phosphorothioate-LNA and 2'-thio-LNAs, have also been prepared (Kumar et al., Bioorg. Med. Chem. Lett., 1998, 8, 2219-2222). Preparation of locked nucleoside analogs containing oligodeoxyribonucleotide duplexes as substrates for nucleic acid polymerases has also been described (Wengel et al., PCT International Application WO 98-DK393 19980914). Furthermore, synthesis of 2'-amino-LNA, a novel conformationally restricted high-affinity oligonucleotide analog with a handle has been described in the art (Singh et al., J. Org. Chem., 1998, 63, 10035-10039). In addition, 2'-Amino- and 2'-methylamino-LNA's have been prepared and the thermal stability of their duplexes with complementary RNA and DNA strands has been previously reported.

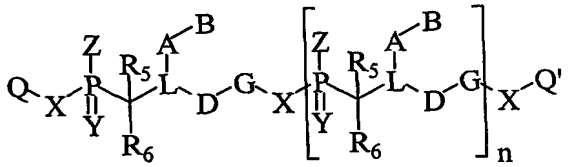
Further oligonucleotide mimetics have been prepared to include bicyclic and tricyclic nucleoside analogs having the formulas (amidite monomers shown):



(see Steffens *et al.*, *Helv. Chim. Acta*, **1997**, *80*, 2426-2439; Steffens *et al.*, *J. Am. Chem. Soc.*, **1999**, *121*, 3249-3255; and Renneberg *et al.*, *J. Am. Chem. Soc.*, **2002**, *124*, 5993-6002). These modified nucleoside analogs have been oligomerized using the phosphoramidite approach and the resulting oligomeric compounds containing tricyclic nucleoside analogs have shown increased thermal stabilities (Tm's) when hybridized to DNA, RNA and itself. Oligomeric compounds containing bicyclic nucleoside analogs have shown thermal stabilities approaching that of DNA duplexes.

Another class of oligonucleotide mimetic is referred to as phosphonomonoester nucleic acids incorporate a phosphorus group in a backbone the backbone. This class of olignucleotide mimetic is reported to have useful physical and biological and pharmacological properties in the areas of inhibiting gene expression (antisense oligonucleotides, ribozymes, sense oligonucleotides and triplex-forming oligonucleotides), as probes for the detection of nucleic acids and as auxiliaries for use in molecular biology.

The general formula (for definitions of Markush variables see: United States Patents 5,874,553 and 6,127,346 herein incorporated by reference in their entirety) is shown below.



Another oligonucleotide mimetic has been reported wherein the furanosyl ring has been replaced by a cyclobutyl moiety.

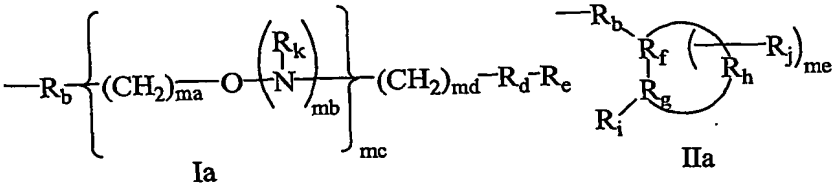
Modified sugars

Oligomeric compounds of the invention may also contain one or more substituted sugar moieties. Preferred oligomeric compounds comprise a sugar substituent group selected from: OH; F; O-, S-, or N-alkyl; O-, S-, or N-alkenyl; O-, S- or N-alkynyl; or O-alkyl-O-alkyl, wherein the alkyl, alkenyl and alkynyl may be substituted or unsubstituted C_1 to C_{10} alkyl or C_2 to C_{10} alkenyl and alkynyl. Particularly preferred are $O[(CH_2)_nO]_mCH_3$, $O(CH_2)_nOCH_3$, $O(CH_2)_nNH_2$, $O(CH_2)_nCH_3$, $O(CH_2)_nONH_2$, and $O(CH_2)_nON[(CH_2)_nCH_3]_2$, where n and m are from 1 to about 10. Other preferred oligonucleotides comprise a sugar substituent group selected from: C_1 to C_{10} lower alkyl, substituted lower alkyl, alkenyl, alkynyl, alkaryl, aralkyl, O-alkaryl or O-aralkyl, SH, SCH_3, OCN, Cl, Br, CN, CF_3, OCF_3, $SOCH_3$, SO_2CH_3, ONO_2, NO_2, N_3, NH_2, heterocycloalkyl, heterocycloalkaryl,

aminoalkylamino, polyalkylamino, substituted silyl, an RNA cleaving group, a reporter group, an intercalator, a group for improving the pharmacokinetic properties of an oligonucleotide, or a group for improving the pharmacodynamic properties of an oligonucleotide, and other substituents having similar properties. A preferred modification includes 2'-methoxyethoxy (2'-O-$CH_2CH_2OCH_3$, also known as 2'-O-(2-methoxyethyl) or 2'-MOE) (Martin *et al.*, *Helv. Chim. Acta*, **1995**, *78*, 486-504) i.e., an alkoxyalkoxy group. A further preferred modification includes 2'-dimethylaminooxyethoxy, i.e., a $O(CH_2)_2ON(CH_3)_2$ group, also known as 2'-DMAOE, as described in examples hereinbelow, and 2'-dimethylamino-ethoxyethoxy (also known in the art as 2'-O-dimethyl-amino-ethoxy-ethyl or 2'-DMAEOE), i.e., 2'-O-CH_2-O-CH_2-$N(CH_3)_2$.

Other preferred sugar substituent groups include methoxy (-O-CH_3), aminopropoxy (-$OCH_2CH_2CH_2NH_2$), allyl (-CH_2-CH=CH_2), -O-allyl (-O-CH_2-CH=CH_2) and fluoro (F). 2'-Sugar substituent groups may be in the arabino (up) position or ribo (down) position. A preferred 2'-arabino modification is 2'-F. Similar modifications may also be made at other positions on the oligomeric compound, particularly the 3' position of the sugar on the 3' terminal nucleoside or in 2'-5' linked oligonucleotides and the 5' position of 5' terminal nucleotide. Oligomeric compounds may also have sugar mimetics such as cyclobutyl moieties in place of the pentofuranosyl sugar. Representative United States patents that teach the preparation of such modified sugar structures include, but are not limited to, U.S.: 4,981,957; 5,118,800; 5,319,080; 5,359,044; 5,393,878; 5,446,137; 5,466,786; 5,514,785; 5,519,134; 5,567,811; 5,576,427; 5,591,722; 5,597,909; 5,610,300; 5,627,053; 5,639,873; 5,646,265; 5,658,873; 5,670,633; 5,792,747; and 5,700,920, certain of which are commonly owned with the instant application, and each of which is herein incorporated by reference in its entirety.

Further representative sugar substituent groups include groups of formula I_a or II_a:



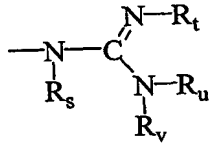
Ia IIa

wherein:

R_b is O, S or NH;

R_d is a single bond, O, S or C(=O);

R_e is C_1-C_{10} alkyl, $N(R_k)(R_m)$, $N(R_k)(R_n)$, $N=C(R_p)(R_q)$, $N=C(R_p)(R_r)$ or has formula III_a;



IIIa

R_p and R_q are each independently hydrogen or C_1-C_{10} alkyl;

R_r is $-R_x-R_y$;

each R_s, R_t, R_u and R_v is, independently, hydrogen, C(O)R_w, substituted or unsubstituted C_1-C_{10} alkyl, substituted or unsubstituted C_2-C_{10} alkenyl, substituted or unsubstituted C_2-C_{10} alkynyl, alkylsulfonyl, arylsulfonyl, a chemical functional group or a conjugate group, wherein the substituent groups are selected from hydroxyl, amino, alkoxy, carboxy, benzyl, phenyl, nitro, thiol, thioalkoxy, halogen, alkyl, aryl, alkenyl and alkynyl;

or optionally, R_u and R_v, together form a phthalimido moiety with the nitrogen atom to which they are attached;

each R_w is, independently, substituted or unsubstituted C_1-C_{10} alkyl, trifluoromethyl, cyanoethyloxy, methoxy, ethoxy, t-butoxy, allyloxy, 9-fluorenylmethoxy, 2-(trimethylsilyl)-ethoxy, 2,2,2-trichloroethoxy, benzyloxy, butyryl, iso-butyryl, phenyl or aryl;

R_k is hydrogen, a nitrogen protecting group or $-R_x-R_y$;

R_p is hydrogen, a nitrogen protecting group or $-R_x-R_y$;

R_x is a bond or a linking moiety;

R_y is a chemical functional group, a conjugate group or a solid support medium;

each R_m and R_n is, independently, H, a nitrogen protecting group, substituted or unsubstituted C_1-C_{10} alkyl, substituted or unsubstituted C_2-C_{10} alkenyl, substituted or unsubstituted C_2-C_{10} alkynyl, wherein the substituent groups are selected from hydroxyl, amino, alkoxy, carboxy, benzyl, phenyl, nitro, thiol, thioalkoxy, halogen, alkyl, aryl, alkenyl, alkynyl; NH_3^+, $N(R_u)(R_v)$, guanidino and acyl where said acyl is an acid amide or an ester;

or R_m and R_n, together, are a nitrogen protecting group, are joined in a ring structure that optionally includes an additional heteroatom selected from N and O or are a chemical functional group;

R_i is OR_z, SR_z, or $N(R_z)_2$;

each R_z is, independently, H, C_1-C_8 alkyl, C_1-C_8 haloalkyl, $C(=NH)N(H)R_u$, $C(=O)N(H)R_u$ or $OC(=O)N(H)R_u$;

R_f, R_g and R_h comprise a ring system having from about 4 to about 7 carbon atoms or having from about 3 to about 6 carbon atoms and 1 or 2 heteroatoms wherein said heteroatoms are selected from oxygen, nitrogen and sulfur and wherein said ring system is aliphatic, unsaturated aliphatic, aromatic, or saturated or unsaturated heterocyclic;

R_j is alkyl or haloalkyl having 1 to about 10 carbon atoms, alkenyl having 2 to about 10 carbon atoms, alkynyl having 2 to about 10 carbon atoms, aryl having 6 to about 14 carbon atoms, $N(R_k)(R_m)$ OR_k, halo, SR_k or CN;

m_a is 1 to about 10;

each mb is, independently, 0 or 1;

mc is 0 or an integer from 1 to 10;

md is an integer from 1 to 10;

me is from 0, 1 or 2; and

provided that when mc is 0, md is greater than 1.

Representative substituents groups of Formula I are disclosed in United States Patent Application Serial No. 09/130,973, filed August 7, 1998, entitled "Capped 2'-Oxyethoxy Oligonucleotides," hereby incorporated by reference in its entirety.

Representative cyclic substituent groups of Formula II are disclosed in United States Patent Application Serial No. 09/123,108, filed July 27, 1998, entitled "RNA Targeted 2'-Oligomeric compounds that are Conformationally Preorganized," hereby incorporated by reference in its entirety.

Particularly preferred sugar substituent groups include $O[(CH_2)_nO]_mCH_3$, $O(CH_2)_nOCH_3$, $O(CH_2)_nNH_2$, $O(CH_2)_nCH_3$, $O(CH_2)_nONH_2$, and $O(CH_2)_nON[(CH_2)_nCH_3)]_2$, where n and m are from 1 to about 10.

Representative guanidino substituent groups that are shown in formula III and IV are disclosed in co-owned United States Patent Application 09/349,040, entitled "Functionalized Oligomers", filed July 7, 1999, hereby incorporated by reference in its entirety.

Representative acetamido substituent groups are disclosed in United States Patent 6,147,200 which is hereby incorporated by reference in its entirety.

Representative dimethylaminoethyloxyethyl substituent groups are disclosed in International Patent Application PCT/US99/17895, entitled "2'-O-Dimethylaminoethyloxyethyl-Oligomeric compounds", filed August 6, 1999, hereby incorporated by reference in its entirety.

Modified Nucleobases/Naturally occurring nucleobases

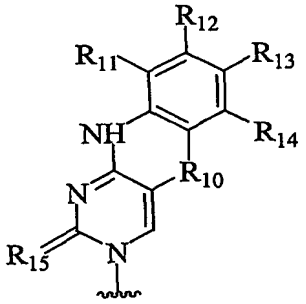
Oligomeric compounds may also include nucleobase (often referred to in the art simply as "base" or "heterocyclic base moiety") modifications or substitutions. As used herein, "unmodified" or "natural" nucleobases include the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C) and uracil (U). Modified nucleobases also

referred herein as heterocyclic base moieties include other synthetic and natural nucleobases such as 5-methylcytosine (5-me-C), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-halouracil and cytosine, 5-propynyl ($-C\equiv C-CH_3$) uracil and cytosine and other alkynyl derivatives of pyrimidine bases, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl and other 8-substituted adenines and guanines, 5-halo particularly 5-bromo, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylguanine and 7-methyladenine, 2-F-adenine, 2-amino-adenine, 8-azaguanine and 8-azaadenine, 7-deazaguanine and 7-deazaadenine and 3-deazaguanine and 3-deazaadenine.

Heterocyclic base moieties may also include those in which the purine or pyrimidine base is replaced with other heterocycles, for example 7-deaza-adenine, 7-deazaguanosine, 2-aminopyridine and 2-pyridone. Further nucleobases include those disclosed in United States Patent No. 3,687,808, those disclosed in *The Concise Encyclopedia Of Polymer Science And Engineering*, pages 858-859, Kroschwitz, J.I., ed. John Wiley & Sons, **1990**, those disclosed by Englisch et al., *Angewandte Chemie*, International Edition, **1991**, *30*, 613, and those disclosed by Sanghvi, Y.S., Chapter 15, *Antisense Research and Applications*, pages 289-302, Crooke, S.T. and Lebleu, B. , ed., CRC Press, **1993**. Certain of these nucleobases are particularly useful for increasing the binding affinity of the oligomeric compounds of the invention. These include 5-substituted pyrimidines, 6-azapyrimidines and N-2, N-6 and O-6 substituted purines, including 2-aminopropyladenine, 5-propynyluracil and 5-propynylcytosine. 5-methylcytosine substitutions have been shown to increase nucleic acid duplex

stability by 0.6-1.2°C (Sanghvi, Y.S., Crooke, S.T. and Lebleu, B., eds., *Antisense Research and Applications*, CRC Press, Boca Raton, **1993**, pp. 276-278) and are presently preferred base substitutions, even more particularly when combined with 2'-O-methoxyethyl sugar modifications.

In one aspect of the present invention oligomeric compounds are prepared having polycyclic heterocyclic compounds in place of one or more heterocyclic base moieties. A number of tricyclic heterocyclic compounds have been previously reported. These compounds are routinely used in antisense applications to increase the binding properties of the modified strand to a target strand. The most studied modifications are targeted to guanosines hence they have been termed G-clamps or cytidine analogs. Many of these polycyclic heterocyclic compounds have the general formula:



Representative cytosine analogs that make 3 hydrogen bonds with a guanosine in a second strand include 1,3-diazaphenoxazine-2-one (R_{10} = O, R_{11} - R_{14}= H) [Kurchavov, *et al.*, *Nucleosides and Nucleotides*, 1997, 16, 1837-1846], 1,3-diazaphenothiazine-2-one (R_{10}= S, R_{11} - R_{14}= H), [Lin, K.-Y.; Jones, R. J.; Matteucci, M. J. Am. Chem. Soc. 1995, 117, 3873-3874] and 6,7,8,9-tetrafluoro-1,3-diazaphenoxazine-2-one (R_{10} = O, R_{11} - R_{14} = F) [Wang, J.; Lin, K.-Y., Matteucci, M. Tetrahedron Lett. 1998, 39, 8385-8388]. Incorporated into oligonucleotides these base modifications were shown to

hybridize with complementary guanine and the latter was also shown to hybridize with adenine and to enhance helical thermal stability by extended stacking interactions(also see U.S. Patent Application entitled "Modified Peptide Nucleic Acids" filed May 24, 2002, Serial number 10/155,920; and U.S. Patent Application entitled "Nuclease Resistant Chimeric Oligonucleotides" filed May 24, 2002, Serial number 10/013,295, both of which are commonly owned with this application and are herein incorporated by reference in their entirety).

Further helix-stabilizing properties have been observed when a cytosine analog/substitute has an aminoethoxy moiety attached to the rigid 1,3-diazaphenoxazine-2-one scaffold (R_{10} = O, R_{11} = -O-$(CH_2)_2$-NH_2, R_{12-14}=H) [Lin, K.-Y.; Matteucci, M. J. Am. Chem. Soc. 1998, 120, 8531-8532]. Binding studies demonstrated that a single incorporation could enhance the binding affinity of a model oligonucleotide to its complementary target DNA or RNA with a ΔT_m of up to 18° relative to 5-methyl cytosine ($dC5^{me}$), which is the highest known affinity enhancement for a single modification, yet. On the other hand, the gain in helical stability does not compromise the specificity of the oligonucleotides. The T_m data indicate an even greater discrimination between the perfect match and mismatched sequences compared to $dC5^{me}$. It was suggested that the tethered amino group serves as an additional hydrogen bond donor to interact with the Hoogsteen face, namely the O6, of a complementary guanine thereby forming 4 hydrogen bonds. This means that the increased affinity of G-clamp is mediated by the combination of extended base stacking and additional specific hydrogen bonding.

Further tricyclic heterocyclic compounds and methods of using them that are amenable to the present invention are disclosed in United States Patent Serial Number 6,028,183, which issued on May 22, 2000, and United States Patent Serial

Number 6,007,992, which issued on December 28, 1999, the contents of both are commonly assigned with this application and are incorporated herein in their entirety.

The enhanced binding affinity of the phenoxazine derivatives together with their uncompromised sequence specificity makes them valuable nucleobase analogs for the development of more potent antisense-based drugs. In fact, promising data have been derived from in vitro experiments demonstrating that heptanucleotides containing phenoxazine substitutions are capable to activate RNaseH, enhance cellular uptake and exhibit an increased antisense activity [Lin, K-Y; Matteucci, M. J. Am. Chem. Soc. 1998, 120, 8531-8532]. The activity enhancement was even more pronounced in case of G-clamp, as a single substitution was shown to significantly improve the in vitro potency of a 20mer 2'-deoxyphosphorothioate oligonucleotides [Flanagan, W. M.; Wolf, J.J.; Olson, P.; Grant, D.; Lin, K.-Y.; Wagner, R. W.; Matteucci, M. Proc. Natl. Acad. Sci. USA, 1999, 96, 3513-3518]. Nevertheless, to optimize oligonucleotide design and to better understand the impact of these heterocyclic modifications on the biological activity, it is important to evaluate their effect on the nuclease stability of the oligomers.

Further modified polycyclic heterocyclic compounds useful as heterocyclcic bases are disclosed in but not limited to, the above noted U.S. 3,687,808, as well as U.S.: 4,845,205; 5,130,302; 5,134,066; 5,175,273; 5,367,066; 5,432,272; 5,434,257; 5,457,187; 5,459,255; 5,484,908; 5,502,177; 5,525,711; 5,552,540; 5,587,469; 5,594,121, 5,596,091; 5,614,617; 5,645,985; 5,646,269; 5,750,692; 5,830,653; 5,763,588; 6,005,096; and 5,681,941, and Unites States Patent Application Serial number 09/996,292 filed November 28, 2001, certain of which are commonly owned with the instant application, and each of which is herein incorporated by reference.

The oligonucleotides of the present invention also include variants in which a different base is present at one or more of the nucleotide positions in the oligonucleotide. For example, if the first nucleotide is an adenosine, variants may be produced which contain thymidine, guanosine or cytidine at this position. This may be done at any of the positions of the oligonucleotide. Thus, a 20-mer may comprise 60 variations (20 positions x 3 alternates at each position) in which the original nucleotide is substituted with any of the three alternate nucleotides. These oligonucleotides are then tested using the methods described herein to determine their ability to inhibit expression of HCV mRNA and/or HCV replication.

Conjugates

A further preferred substitution that can be appended to the oligomeric compounds of the invention involves the linkage of one or more moieties or conjugates which enhance the activity, cellular distribution or cellular uptake of the resulting oligomeric compounds. In one embodiment such modified oligomeric compounds are prepared by covalently attaching conjugate groups to functional groups such as hydroxyl or amino groups. Conjugate groups of the invention include intercalators, reporter molecules, polyamines, polyamides, polyethylene glycols, polyethers, groups that enhance the pharmacodynamic properties of oligomers, and groups that enhance the pharmacokinetic properties of oligomers. Typical conjugates groups include cholesterols, lipids, phospholipids, biotin, phenazine, folate, phenanthridine, anthraquinone, acridine, fluoresceins, rhodamines, coumarins, and dyes. Groups that enhance the pharmacodynamic properties, in the context of this invention, include groups that improve oligomer uptake, enhance oligomer resistance to degradation, and/or strengthen sequence-specific hybridization with RNA. Groups that enhance the pharmacokinetic properties, in the context of this invention, include groups that improve

oligomer uptake, distribution, metabolism or excretion. Representative conjugate groups are disclosed in International Patent Application PCT/US92/09196, filed October 23, 1992 the entire disclosure of which is incorporated herein by reference. Conjugate moieties include but are not limited to lipid moieties such as a cholesterol moiety (Letsinger et al., *Proc. Natl. Acad. Sci. USA*, **1989**, *86*, 6553-6556), cholic acid (Manoharan et al., *Bioorg. Med. Chem. Let.*, **1994**, *4*, 1053-1060), a thioether, e.g., hexyl-S-tritylthiol (Manoharan et al., *Ann. N.Y. Acad. Sci.*, **1992**, *660*, 306-309; Manoharan et al., *Bioorg. Med. Chem. Let.*, **1993**, *3*, 2765-2770), a thiocholesterol (Oberhauser et al., *Nucl. Acids Res.*, **1992**, *20*, 533-538), an aliphatic chain, e.g., dodecandiol or undecyl residues (Saison-Behmoaras et al., *EMBO J.*, **1991**, *10*, 1111-1118; Kabanov et al., *FEBS Lett.*, **1990**, *259*, 327-330; Svinarchuk et al., *Biochimie*, **1993**, *75*, 49-54), a phospholipid, e.g., di-hexadecyl-rac-glycerol or triethyl-ammonium 1,2-di-O-hexadecyl-rac-glycero-3-H-phosphonate (Manoharan et al., *Tetrahedron Lett.*, **1995**, *36*, 3651-3654; Shea et al., *Nucl. Acids Res.*, **1990**, *18*, 3777-3783), a polyamine or a polyethylene glycol chain (Manoharan et al., *Nucleosides & Nucleotides*, **1995**, *14*, 969-973), or adamantane acetic acid (Manoharan et al., *Tetrahedron Lett.*, **1995**, *36*, 3651-3654), a palmityl moiety (Mishra et al., *Biochim. Biophys. Acta*, **1995**, *1264*, 229-237), or an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety (Crooke et al., *J. Pharmacol. Exp. Ther.*, **1996**, *277*, 923-937.

The oligomeric compounds of the invention may also be conjugated to active drug substances, for example, aspirin, warfarin, phenylbutazone, ibuprofen, suprofen, fenbufen, ketoprofen, (*S*)-(+)-pranoprofen, carprofen, dansylsarcosine, 2,3,5-triiodobenzoic acid, flufenamic acid, folinic acid, a benzothiadiazide, chlorothiazide, a diazepine, indomethicin, a barbiturate, a cephalosporin, a sulfa drug, an antidiabetic,

an antibacterial or an antibiotic. Oligonucleotide-drug conjugates and their preparation are described in United States Patent Application 09/334,130 (filed June 15, 1999) which is incorporated herein by reference in its entirety.

Representative United States patents that teach the preparation of such oligonucleotide conjugates include, but are not limited to, U.S.: 4,828,979; 4,948,882; 5,218,105; 5,525,465; 5,541,313; 5,545,730; 5,552,538; 5,578,717, 5,580,731; 5,580,731; 5,591,584; 5,109,124; 5,118,802; 5,138,045; 5,414,077; 5,486,603; 5,512,439; 5,578,718; 5,608,046; 4,587,044; 4,605,735; 4,667,025; 4,762,779; 4,789,737; 4,824,941; 4,835,263; 4,876,335; 4,904,582; 4,958,013; 5,082,830; 5,112,963; 5,214,136; 5,082,830; 5,112,963; 5,214,136; 5,245,022; 5,254,469; 5,258,506; 5,262,536; 5,272,250; 5,292,873; 5,317,098; 5,371,241, 5,391,723; 5,416,203, 5,451,463; 5,510,475; 5,512,667; 5,514,785; 5,565,552; 5,567,810; 5,574,142; 5,585,481; 5,587,371; 5,595,726; 5,597,696; 5,599,923; 5,599,928 and 5,688,941, certain of which are commonly owned with the instant application, and each of which is herein incorporated by reference.

Chimeric oligomeric compounds

It is not necessary for all positions in an oligomeric compound to be uniformly modified, and in fact more than one of the aforementioned modifications may be incorporated in a single oligomeric compound or even at a single monomeric subunit such as a nucleoside within a oligomeric compound. The present invention also includes oligomeric compounds which are chimeric oligomeric compounds. "Chimeric" oligomeric compounds or "chimeras," in the context of this invention, are oligomeric compounds that contain two or more chemically distinct regions, each made up of at least one monomer unit, i.e., a nucleotide in the case of a nucleic acid based

oligomer.

Chimeric oligomeric compounds typically contain at least one region modified so as to confer increased resistance to nuclease degradation, increased cellular uptake, and/or increased binding affinity for the target nucleic acid. An additional region of the oligomeric compound may serve as a substrate for enzymes capable of cleaving RNA:DNA or RNA:RNA hybrids. By way of example, RNase H is a cellular endonuclease which cleaves the RNA strand of an RNA:DNA duplex. Activation of RNase H, therefore, results in cleavage of the RNA target, thereby greatly enhancing the efficiency of inhibition of gene expression. Consequently, comparable results can often be obtained with shorter oligomeric compounds when chimeras are used, compared to for example phosphorothioate deoxyoligonucleotides hybridizing to the same target region. Cleavage of the RNA target can be routinely detected by gel electrophoresis and, if necessary, associated nucleic acid hybridization techniques known in the art.

Chimeric oligomeric compounds of the invention may be formed as composite structures of two or more oligonucleotides, oligonucleotide analogs, oligonucleosides and/or oligonucleotide mimetics as described above. Such oligomeric compounds have also been referred to in the art as hybrids hemimers, gapmers or inverted gapmers. Representative United States patents that teach the preparation of such hybrid structures include, but are not limited to, U.S.: 5,013,830; 5,149,797; 5,220,007; 5,256,775; 5,366,878; 5,403,711; 5,491,133; 5,565,350; 5,623,065; 5,652,355; 5,652,356; and 5,700,922, certain of which are commonly owned with the instant application, and each of which is herein incorporated by reference in its entirety.

3'-endo modifications

In one aspect of the present invention oligomeric compounds include nucleosides synthetically modified to induce

a 3'-endo sugar conformation. A nucleoside can incorporate synthetic modifications of the heterocyclic base, the sugar moiety or both to induce a desired 3'-endo sugar conformation. These modified nucleosides are used to mimic RNA like nucleosides so that particular properties of an oligomeric compound can be enhanced while maintaining the desirable 3'-endo conformational geometry. There is an apparent preference for an RNA type duplex (A form helix, predominantly 3'-endo) as a requirement (e.g. trigger) of RNA interference which is supported in part by the fact that duplexes composed of 2'-deoxy-2'-F-nucleosides appears efficient in triggering RNAi response in the *C. elegans* system. Properties that are enhanced by using more stable 3'-endo nucleosides include but aren't limited to modulation of pharmacokinetic properties through modification of protein binding, protein off-rate, absorption and clearance; modulation of nuclease stability as well as chemical stability; modulation of the binding affinity and specificity of the oligomer (affinity and specificity for enzymes as well as for complementary sequences); and increasing efficacy of RNA cleavage. The present invention provides oligomeric triggers of RNAi having one or more nucleosides modified in such a way as to favor a C3'-endo type conformation.

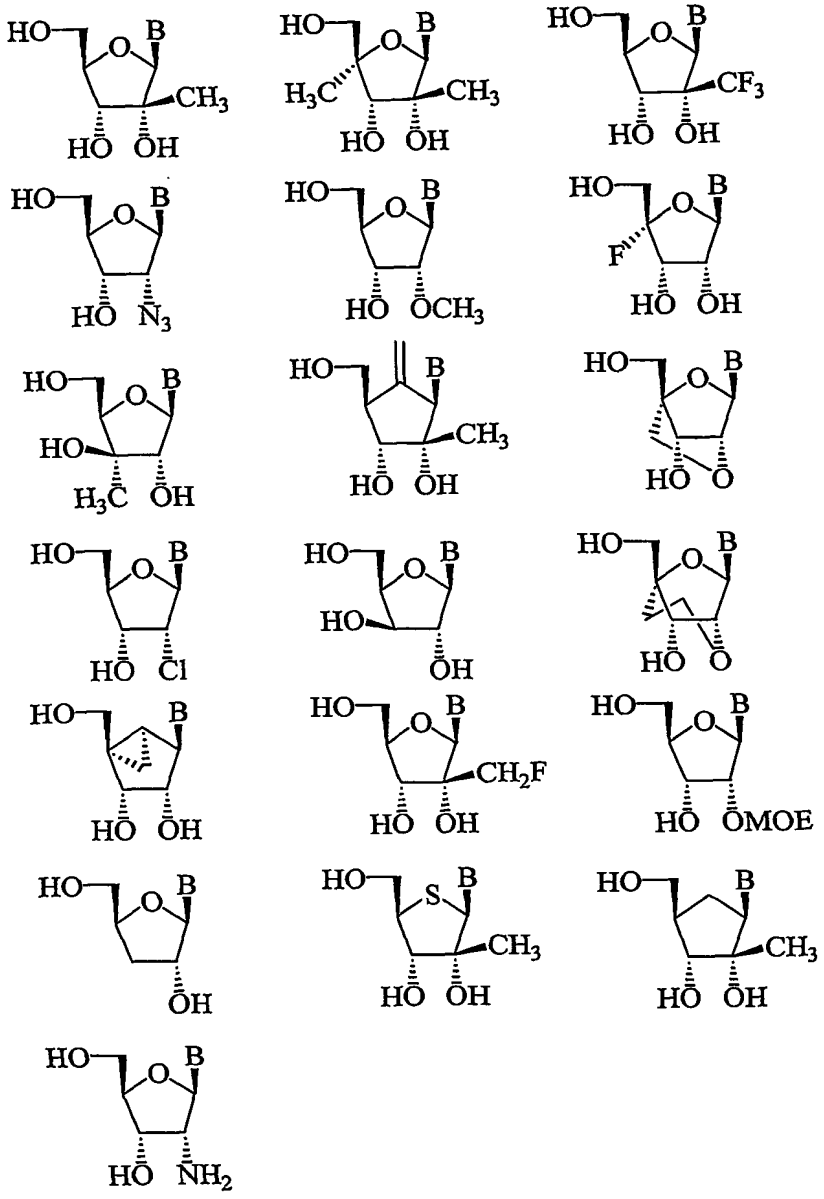
Scheme 1

C2'-endo/Southern C3'-endo/Northern

Nucleoside conformation is influenced by various factors including substitution at the 2', 3' or 4'-positions of the pentofuranosyl sugar. Electronegative substituents generally prefer the axial positions, while sterically demanding

substituents generally prefer the equatorial positions (Principles of Nucleic Acid Structure, Wolfgang Sanger, 1984, Springer-Verlag.) Modification of the 2' position to favor the 3'-endo conformation can be achieved while maintaining the 2'-OH as a recognition element, as illustrated in Figure 2, below (Gallo et al., Tetrahedron (2001), 57, 5707-5713. Harry-O'kuru et al., J. Org. Chem., (1997), 62(6), 1754-1759 and Tang et al., J. Org. Chem. (1999), 64, 747-754.) Alternatively, preference for the 3'-endo conformation can be achieved by deletion of the 2'-OH as exemplified by 2'deoxy-2'F-nucleosides (Kawasaki et al., J. Med. Chem. (1993), 36, 831-841), which adopts the 3'-endo conformation positioning the electronegative fluorine atom in the axial position. Other modifications of the ribose ring, for example substitution at the 4'-position to give 4'-F modified nucleosides (Guillerm et al., Bioorganic and Medicinal Chemistry Letters (1995), 5, 1455-1460 and Owen et al., J. Org. Chem. (1976), 41, 3010-3017), or for example modification to yield methanocarba nucleoside analogs (Jacobson et al., J. Med. Chem. Lett. (2000), 43, 2196-2203 and Lee et al., Bioorganic and Medicinal Chemistry Letters (2001), 11, 1333-1337) also induce preference for the 3'-endo conformation. Along similar lines, oligomeric triggers of RNAi response might be composed of one or more nucleosides modified in such a way that conformation is locked into a C3'-endo type conformation, i.e. Locked Nucleic Acid (LNA, Singh et al, Chem. Commun. (1998), 4, 455-456), and ethylene bridged Nucleic Acids (ENA, Morita et al, Bioorganic & Medicinal Chemistry Letters (2002), 12, 73-76.) Examples of modified nucleosides amenable to the present invention are shown below in Table I. These examples are meant to be representative and not exhaustive.

Table I



The preferred conformation of modified nucleosides and their oligomers can be estimated by various methods such as molecular dynamics calculations, nuclear magnetic resonance spectroscopy and CD measurements. Hence, modifications predicted to induce RNA like conformations, A-form duplex

geometry in an oligomeric context, are selected for use in the modified oligoncleotides of the present invention. The synthesis of numerous modified nucleosides amenable to the present invention are known in the art (see for example, Chemistry of Nucleosides and Nucleotides Vol 1-3, ed. Leroy B. Townsend, 1988, Plenum press., and the examples section below.)

In one aspect, the present invention is directed to oligonucleotides that are prepared having enhanced properties compared to native RNA against nucleic acid targets. A target is identified and an oligonucleotide is selected having an effective length and sequence that is complementary to a portion of the target sequence. Each nucleoside of the selected sequence is scrutinized for possible enhancing modifications. A preferred modification would be the replacement of one or more RNA nucleosides with nucleosides that have the same 3'-endo conformational geometry. Such modifications can enhance chemical and nuclease stability relative to native RNA while at the same time being much cheaper and easier to synthesize and/or incorporate into an oligonulceotide. The selected sequence can be further divided into regions and the nucleosides of each region evaluated for enhancing modifications that can be the result of a chimeric configuration. Consideration is also given to the 5' and 3'-termini as there are often advantageous modifications that can be made to one or more of the terminal nucleosides. The oligomeric compounds of the present invention include at least one 5'-modified phosphate group on a single strand or on at least one 5'-position of a double stranded sequence or sequences. Further modifications are also considered such as internucleoside linkages, conjugate groups, substitute sugars or bases, substitution of one or more nucleosides with nucleoside mimetics and any other modification that can enhance the selected sequence for its intended target. The terms used to

describe the conformational geometry of homoduplex nucleic acids are "A Form" for RNA and "B Form" for DNA. The respective conformational geometry for RNA and DNA duplexes was determined from X-ray diffraction analysis of nucleic acid fibers (Arnott and Hukins, *Biochem. Biophys. Res. Comm.*, **1970**, 47, 1504.) In general, RNA:RNA duplexes are more stable and have higher melting temperatures (Tm's) than DNA:DNA duplexes (Sanger et al., Principles of Nucleic Acid Structure, 1984, Springer-Verlag; New York, NY.; Lesnik et al., Biochemistry, 1995, 34, 10807-10815; Conte et al., Nucleic Acids Res., 1997, 25, 2627-2634). The increased stability of RNA has been attributed to several structural features, most notably the improved base stacking interactions that result from an A-form geometry (Searle et al., Nucleic Acids Res., 1993, 21, 2051-2056). The presence of the 2' hydroxyl in RNA biases the sugar toward a C3' endo pucker, i.e., also designated as Northern pucker, which causes the duplex to favor the A-form geometry. In addition, the 2' hydroxyl groups of RNA can form a network of water mediated hydrogen bonds that help stabilize the RNA duplex (Egli et al., Biochemistry, 1996, 35, 8489-8494). On the other hand, deoxy nucleic acids prefer a C2' endo sugar pucker, i.e., also known as Southern pucker, which is thought to impart a less stable B-form geometry (Sanger, W. (1984) Principles of Nucleic Acid Structure, Springer-Verlag, New York, NY). As used herein, B-form geometry is inclusive of both C2'-endo pucker and O4'-endo pucker. This is consistent with Berger, *et. al.*, *Nucleic Acids Research*, **1998**, *26*, 2473-2480, who pointed out that in considering the furanose conformations which give rise to B-form duplexes consideration should also be given to a O4'-endo pucker contribution.

DNA:RNA hybrid duplexes, however, are usually less stable than pure RNA:RNA duplexes, and depending on their sequence may be either more or less stable than DNA:DNA duplexes

(Searle *et al.*, *Nucleic Acids Res.*, **1993**, *21*, 2051-2056). The structure of a hybrid duplex is intermediate between A- and B-form geometries, which may result in poor stacking interactions (Lane *et al.*, *Eur. J. Biochem.*, **1993**, *215*, 297-306; Fedoroff *et al.*, *J. Mol. Biol.*, **1993**, *233*, 509-523; Gonzalez *et al.*, *Biochemistry*, **1995**, *34*, 4969-4982; Horton *et al.*, *J. Mol. Biol.*, **1996**, *264*, 521-533). The stability of the duplex formed between a target RNA and a synthetic sequence is central to therapies such as but not limited to antisense and RNA interference as these mechanisms require the binding of a synthetic oligonucleotide strand to an RNA target strand. In the case of antisense, effective inhibition of the mRNA requires that the antisense DNA have a very high binding affinity with the mRNA. Otherwise the desired interaction between the synthetic oligonucleotide strand and target mRNA strand will occur infrequently, resulting in decreased efficacy.

One routinely used method of modifying the sugar puckering is the substitution of the sugar at the 2'-position with a substituent group that influences the sugar geometry. The influence on ring conformation is dependant on the nature of the substituent at the 2'-position. A number of different substituents have been studied to determine their sugar puckering effect. For example, 2'-halogens have been studied showing that the 2'-fluoro derivative exhibits the largest population (65%) of the C3'-endo form, and the 2'-iodo exhibits the lowest population (7%). The populations of adenosine (2'-OH) versus deoxyadenosine (2'-H) are 36% and 19%, respectively. Furthermore, the effect of the 2'-fluoro group of adenosine dimers (2'-deoxy-2'-fluoroadenosine - 2'-deoxy-2'-fluoro-adenosine) is further correlated to the stabilization of the stacked conformation.

As expected, the relative duplex stability can be enhanced by replacement of 2'-OH groups with 2'-F groups

thereby increasing the C3'-endo population. It is assumed that the highly polar nature of the 2'-F bond and the extreme preference for C3'-endo puckering may stabilize the stacked conformation in an A-form duplex. Data from UV hypochromicity, circular dichroism, and ^{1}H NMR also indicate that the degree of stacking decreases as the electronegativity of the halo substituent decreases. Furthermore, steric bulk at the 2'-position of the sugar moiety is better accommodated in an A-form duplex than a B-form duplex. Thus, a 2'-substituent on the 3'-terminus of a dinucleoside monophosphate is thought to exert a number of effects on the stacking conformation: steric repulsion, furanose puckering preference, electrostatic repulsion, hydrophobic attraction, and hydrogen bonding capabilities. These substituent effects are thought to be determined by the molecular size, electronegativity, and hydrophobicity of the substituent. Melting temperatures of complementary strands is also increased with the 2'-substituted adenosine diphosphates. It is not clear whether the 3'-endo preference of the conformation or the presence of the substituent is responsible for the increased binding. However, greater overlap of adjacent bases (stacking) can be achieved with the 3'-endo conformation.

One synthetic 2'-modification that imparts increased nuclease resistance and a very high binding affinity to nucleotides is the 2-methoxyethoxy (2'-MOE, 2'-$OCH_2CH_2OCH_3$) side chain (Baker *et al.*, *J. Biol. Chem.*, **1997**, *272*, 11944-12000). One of the immediate advantages of the 2'-MOE substitution is the improvement in binding affinity, which is greater than many similar 2' modifications such as *O*-methyl, *O*-propyl, and O-aminopropyl. Oligonucleotides having the 2'-*O*-methoxyethyl substituent also have been shown to be antisense inhibitors of gene expression with promising features for *in vivo* use (Martin, P., *Helv. Chim. Acta*, **1995**,

78, 486-504; Altmann *et al.*, *Chimia*, **1996**, *50*, 168-176; Altmann *et al.*, *Biochem. Soc. Trans.*, **1996**, *24*, 630-637; and Altmann *et al.*, *Nucleosides Nucleotides*, 1997, *16*, 917-926). Relative to DNA, the oligonucleotides having the 2'-MOE modification displayed improved RNA affinity and higher nuclease resistance. Chimeric oligonucleotides having 2'-MOE substituents in the wing nucleosides and an internal region of deoxy-phosphorothioate nucleotides (also termed a gapped oligonucleotide or gapmer) have shown effective reduction in the growth of tumors in animal models at low doses. 2'-MOE substituted oligonucleotides have also shown outstanding promise as antisense agents in several disease states. One such MOE substituted oligonucleotide is presently being investigated in clinical trials for the treatment of CMV retinitis.

Chemistries Defined

Unless otherwise defined herein, alkyl means C_1-C_{12}, preferably C_1-C_8, and more preferably C_1-C_6, straight or (where possible) branched chain aliphatic hydrocarbyl.

Unless otherwise defined herein, heteroalkyl means C_1-C_{12}, preferably C_1-C_8, and more preferably C_1-C_6, straight or (where possible) branched chain aliphatic hydrocarbyl containing at least one, and preferably about 1 to about 3, hetero atoms in the chain, including the terminal portion of the chain. Preferred heteroatoms include N, O and S. Unless otherwise defined herein, cycloalkyl means C_3-C_{12}, preferably C_3-C_8, and more preferably C_3-C_6, aliphatic hydrocarbyl ring.

Unless otherwise defined herein, alkenyl means C_2-C_{12}, preferably C_2-C_8, and more preferably C_2-C_6 alkenyl, which may be straight or (where possible) branched hydrocarbyl moiety, which contains at least one carbon-carbon double bond.

Unless otherwise defined herein, alkynyl means C_2-C_{12}, preferably C_2-C_8, and more preferably C_2-C_6 alkynyl, which may

be straight or (where possible) branched hydrocarbyl moiety, which contains at least one carbon-carbon triple bond.

Unless otherwise defined herein, heterocycloalkyl means a ring moiety containing at least three ring members, at least one of which is carbon, and of which 1, 2 or three ring members are other than carbon. Preferably the number of carbon atoms varies from 1 to about 12, preferably 1 to about 6, and the total number of ring members varies from three to about 15, preferably from about 3 to about 8. Preferred ring heteroatoms are N, O and S. Preferred heterocycloalkyl groups include morpholino, thiomorpholino, piperidinyl, piperazinyl, homopiperidinyl, homopiperazinyl, homomorpholino, homothiomorpholino, pyrrolodinyl, tetrahydrooxazolyl, tetrahydroimidazolyl, tetrahydrothiazolyl, tetrahydroisoxazolyl, tetrahydropyrrazolyl, furanyl, pyranyl, and tetrahydroisothiazolyl.

Unless otherwise defined herein, aryl means any hydrocarbon ring structure containing at least one aryl ring. Preferred aryl rings have about 6 to about 20 ring carbons. Especially preferred aryl rings include phenyl, napthyl, anthracenyl, and phenanthrenyl.

Unless otherwise defined herein, hetaryl means a ring moiety containing at least one fully unsaturated ring, the ring consisting of carbon and non-carbon atoms. Preferably the ring system contains about 1 to about 4 rings. Preferably the number of carbon atoms varies from 1 to about 12, preferably 1 to about 6, and the total number of ring members varies from three to about 15, preferably from about 3 to about 8. Preferred ring heteroatoms are N, O and S. Preferred hetaryl moieties include pyrazolyl, thiophenyl, pyridyl, imidazolyl, tetrazolyl, pyridyl, pyrimidinyl, purinyl, quinazolinyl, quinoxalinyl, benzimidazolyl, benzothiophenyl, etc.

Unless otherwise defined herein, where a moiety is defined as a compound moiety, such as hetarylalkyl (hetaryl

and alkyl), aralkyl (aryl and alkyl), etc., each of the sub-moieties is as defined herein.

Unless otherwise defined herein, an electron withdrawing group is a group, such as the cyano or isocyanato group that draws electronic charge away from the carbon to which it is attached. Other electron withdrawing groups of note include those whose electronegativities exceed that of carbon, for example halogen, nitro, or phenyl substituted in the ortho- or para-position with one or more cyano, isothiocyanato, nitro or halo groups.

Unless otherwise defined herein, the terms halogen and halo have their ordinary meanings. Preferred halo (halogen) substituents are Cl, Br, and I.

The aforementioned optional substituents are, unless otherwise herein defined, suitable substituents depending upon desired properties. Included are halogens (Cl, Br, I), alkyl, alkenyl, and alkynyl moieties, NO_2, NH_3 (substituted and unsubstituted), acid moieties (e.g. $-CO_2H$, $-OSO_3H_2$, etc.), heterocycloalkyl moieties, hetaryl moieties, aryl moieties, etc. In all the preceding formulae, the squiggle (~) indicates a bond to an oxygen or sulfur of the 5'-phosphate.

Phosphate protecting groups include those described in US Patents No. US 5,760,209, US 5,614,621, US 6,051,699, US 6,020,475, US 6,326,478, US 6,169,177, US 6,121,437, US 6,465,628 each of which is expressly incorporated herein by reference in its entirety.

The oligonucleotides in accordance with this invention (single stranded or double stranded) preferably comprise from about 8 to about 80 nucleotides, more preferably from about 12-50 nucleotides and most preferably from about 15 to 30 nucleotides. As is known in the art, a nucleotide is a base-sugar combination suitably bound to an adjacent nucleotide through a phosphodiester, phosphorothioate or other covalent linkage.

The oligonucleotides of the present invention also include variants in which a different base is present at one or more of the nucleotide positions in the oligonucleotide. For example, if the first nucleotide is an adenosine, variants may be produced which contain thymidine, guanosine or cytidine at this position. This may be done at any of the positions of the oligonucleotide. Thus, a 20-mer may comprise 60 variations (20 positions x 3 alternates at each position) in which the original nucleotide is substituted with any of the three alternate nucleotides. These oligonucleotides are then tested using the methods described herein to determine their ability to inhibit expression of p38α MAP kinase mRNA.

The oligonucleotides used in accordance with this invention may be conveniently and routinely made through the well-known technique of solid phase synthesis. Equipment for such synthesis is sold by several vendors including Applied Biosystems. Any other means for such synthesis may also be employed; the actual synthesis of the oligonucleotides is well within the talents of the routineer. It is well known to use similar techniques to prepare oligonucleotides such as the phosphorothioates and 2'-alkoxy or 2'-alkoxyalkoxy derivatives, including 2'-O-methoxyethyl oligonucleotides [Martin, P., *Helv. Chim. Acta*, 78, 486 (1995)]. It is also well known to use similar techniques and commercially available modified amidites and controlled-pore glass (CPG) products such as biotin, fluorescein, acridine or psoralen-modified amidites and/or CPG (available from Glen Research, Sterling VA) to synthesize fluorescently labeled, biotinylated or other conjugated oligonucleotides.

The antisense compounds of the present invention include bioequivalent compounds, including pharmaceutically acceptable salts and prodrugs. This is intended to encompass any pharmaceutically acceptable salts, esters, or salts of such esters, or any other compound which, upon administration to an

animal including a human, is capable of providing (directly or indirectly) the biologically active metabolite or residue thereof. Accordingly, for example, the disclosure is also drawn to pharmaceutically acceptable salts of the nucleic acids of the invention and prodrugs of such nucleic acids.

Pharmaceutically acceptable "salts" are physiologically and pharmaceutically acceptable salts of the nucleic acids of the invention: *i.e.*, salts that retain the desired biological activity of the parent compound and do not impart undesired toxicological effects thereto [see, for example, Berge *et al.*, "Pharmaceutical Salts," *J. of Pharma Sci.*, *66*:1 (1977)].

For oligonucleotides, examples of pharmaceutically acceptable salts include but are not limited to (a) salts formed with cations such as sodium, potassium, ammonium, magnesium, calcium, polyamines such as spermine and spermidine, etc.; (b) acid addition salts formed with inorganic acids, for example hydrochloric acid, hydrobromic acid, sulfuric acid, phosphoric acid, nitric acid and the like; (c) salts formed with organic acids such as, for example, acetic acid, oxalic acid, tartaric acid, succinic acid, maleic acid, fumaric acid, gluconic acid, citric acid, malic acid, ascorbic acid, benzoic acid, tannic acid, palmitic acid, alginic acid, polyglutamic acid, naphthalenesulfonic acid, methanesulfonic acid, p-toluenesulfonic acid, naphthalenedisulfonic acid, polygalacturonic acid, and the like; and (d) salts formed from elemental anions such as chlorine, bromine, and iodine.

The oligonucleotides of the invention may additionally or alternatively be prepared to be delivered in a "prodrug" form. The term "prodrug" indicates a therapeutic agent that is prepared in an inactive form that is converted to an active form (i.e., drug) within the body or cells thereof by the action of endogenous enzymes or other chemicals and/or conditions. In particular, prodrug versions of the oligonucleotides of the invention are prepared as SATE

[(S-acetyl-2-thioethyl) phosphate] derivatives according to the methods disclosed in WO 93/24510 to Gosselin et al., published December 9, 1993.

For therapeutic or prophylactic treatment, oligonucleotides are administered in accordance with this invention. Oligonucleotide compounds of the invention may be formulated in a pharmaceutical composition, which may include pharmaceutically acceptable carriers, thickeners, diluents, buffers, preservatives, surface active agents, neutral or cationic lipids, lipid complexes, liposomes, penetration enhancers, carrier compounds and other pharmaceutically acceptable carriers or excipients and the like in addition to the oligonucleotide. Such compositions and formulations are comprehended by the present invention.

Pharmaceutical compositions comprising the oligonucleotides of the present invention may include penetration enhancers in order to enhance the alimentary delivery of the oligonucleotides. Penetration enhancers may be classified as belonging to one of five broad categories, i.e., fatty acids, bile salts, chelating agents, surfactants and non-surfactants (Lee *et al.*, *Critical Reviews in Therapeutic Drug Carrier Systems*, 1991, *8*:91-192; Muranishi, *Critical Reviews in Therapeutic Drug Carrier Systems*, 1990, 7:1). One or more penetration enhancers from one or more of these broad categories may be included.

The compositions of the present invention may additionally contain other adjunct components conventionally found in pharmaceutical compositions, at their art-established usage levels. Thus, for example, the compositions may contain additional compatible pharmaceutically-active materials such as, e.g., antipruritics, astringents, local anesthetics or anti-inflammatory agents, or may contain additional materials useful in physically formulating various dosage forms of the composition of present invention, such as dyes, flavoring agents, preservatives, antioxidants, opacifiers, thickening

agents and stabilizers. However, such materials, when added, should not unduly interfere with the biological activities of the components of the compositions of the invention.

Regardless of the method by which the oligonucleotides of the invention are introduced into a patient, colloidal dispersion systems may be used as delivery vehicles to enhance the *in vivo* stability of the oligonucleotides and/or to target the oligonucleotides to a particular organ, tissue or cell type. Colloidal dispersion systems include, but are not limited to, macromolecule complexes, nanocapsules, microspheres, beads and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, liposomes and lipid:oligonucleotide complexes of uncharacterized structure. A preferred colloidal dispersion system is a plurality of liposomes. Liposomes are microscopic spheres having an aqueous core surrounded by one or more outer layers made up of lipids arranged in a bilayer configuration [see, generally, Chonn et al., *Current Op. Biotech.*, *6*, 698 (1995)].

The pharmaceutical compositions of the present invention may be administered in a number of ways depending upon whether local or systemic treatment is desired and upon the area to be treated. Administration may be topical (including ophthalmic, vaginal, rectal, intranasal, epidermal and transdermal), oral or parenteral. Parenteral administration includes intravenous drip, subcutaneous, intraperitoneal or intramuscular injection, pulmonary administration, e.g., by inhalation or insufflation of powders or aerosols, including by nebulizer, metered dose inhaler or dry powder inhaler; intratracheal, intranasal, or intracranial, e.g., intrathecal or intraventricular, administration. Oligonucleotides with at least one 2'-O-methoxyethyl modification are believed to be particularly useful for oral administration.

Formulations for topical administration may include transdermal patches, ointments, lotions, creams, gels, drops, suppositories, sprays, liquids and powders. Conventional

pharmaceutical carriers, aqueous, powder or oily bases, thickeners and the like may be necessary or desirable. Coated condoms, gloves and the like may also be useful.

Compositions for oral administration include powders or granules, suspensions or solutions in water or non-aqueous media, capsules, sachets or tablets. Thickeners, flavoring agents, diluents, emulsifiers, dispersing aids or binders may be desirable.

Compositions for parenteral administration may include sterile aqueous solutions which may also contain buffers, diluents and other suitable additives. In some cases it may be more effective to treat a patient with an oligonucleotide of the invention in conjunction with other traditional therapeutic modalities in order to increase the efficacy of a treatment regimen. In the context of the invention, the term "treatment regimen" is meant to encompass therapeutic, palliative and prophylactic modalities. For example, a patient may be treated with conventional chemotherapeutic agents, particularly those used for tumor and cancer treatment. Examples of such chemotherapeutic agents include but are not limited to daunorubicin, daunomycin, dactinomycin, doxorubicin, epirubicin, idarubicin, esorubicin, bleomycin, mafosfamide, ifosfamide, cytosine arabinoside, bis-chloroethylnitrosurea, busulfan, mitomycin C, actinomycin D, mithramycin, prednisone, hydroxyprogesterone, testosterone, tamoxifen, dacarbazine, procarbazine, hexamethylmelamine, pentamethylmelamine, mitoxantrone, amsacrine, chlorambucil, methylcyclohexylnitrosurea, nitrogen mustards, melphalan, cyclophosphamide, 6-mercaptopurine, 6-thioguanine, cytarabine (CA), 5-azacytidine, hydroxyurea, deoxycoformycin, 4-hydroxyperoxycyclophosphoramide, 5-fluorouracil (5-FU), 5-fluorodeoxyuridine (5-FUdR), methotrexate (MTX), colchicine,taxol, vincristine, vinblastine, etoposide, trimetrexate, teniposide, cisplatin and diethylstilbestrol (DES). See, generally, *The Merck Manual of Diagnosis and*

Therapy, 15th Ed., pp. 1206-1228, Berkow *et al.*, eds., Rahay, N.J., 1987). When used with the compounds of the invention, such chemotherapeutic agents may be used individually (*e.g.*, 5-FU and oligonucleotide), sequentially (e.g., 5-FU and oligonucleotide for a period of time followed by MTX and oligonucleotide), or in combination with one or more other such chemotherapeutic agents (e.g., 5-FU, MTX and oligonucleotide, or 5-FU, radiotherapy and oligonucleotide).

Antisense inhibitors of p38 mitogen-activated protein kinase, particularly p38α mitogen-activated protein kinase, are shown herein to decrease expression of p38 mitogen-activated protein kinase in cells collected by bronchoalveolar lavage. They are also shown to reduce pulmonary inflammatory responses, airway hyperreactivity and mucus production in an asthma model, as well as modulating cytokine release into the airway. It is therefore believed that antisense inhibitors of p38 mitogen-activated protein kinase, particularly p38α mitogen-activated protein kinase, are useful for decreasing airway hyperresponsiveness or airway inflammation in animals, including humans and thus for treating inflammatory diseases of the airway, such as asthma (including allergic asthma).

The compositions and methods of the present invention may be used to treat airway hyperreactivity and airway inflammation. The combined use of antisense compounds targeted to human p38 MAP kinase with one or more conventional asthma medications including, but not limited to, montelukast sodium (Singulair™), albuterol, beclomethasone dipropionate, triamcinolone acetonide, ipratropium bromide (Atrovent™), flunisolide, fluticasone propionate (Flovent™) and other steroids is also contemplated. The antisense compounds may be given topically into the airway, e.g,. by inhalation of aerosol (such as via a metered dose inhaler) or dry powder. Topical administration into the airway includes intranasal, intratracheal or intrapulmonary administration.

The formulation of therapeutic compositions and their subsequent administration is believed to be within the skill of those in the art. Dosing is dependent on severity and responsiveness of the disease state to be treated, with the course of treatment lasting from several days to several months, or until a cure is effected or a diminution of the disease state is achieved. Optimal dosing schedules can be calculated from measurements of drug accumulation in the body of the patient. Persons of ordinary skill can easily determine optimum dosages, dosing methodologies and repetition rates. Optimum dosages may vary depending on the relative potency of individual oligonucleotides, and can generally be estimated based on EC_{50}s found to be effective in *in vitro* and *in vivo* animal models. In general, dosage is from 0.01 μg to 100 g per kg of body weight, and may be given once or more daily, weekly, monthly or yearly, or even once every 2 to 20 years. Persons of ordinary skill in the art can easily estimate repetition rates for dosing based on measured residence times and concentrations of the drug in bodily fluids or tissues. Following successful treatment, it may be desirable to have the patient undergo maintenance therapy to prevent the recurrence of the disease state, wherein the oligonucleotide is administered in maintenance doses, ranging from 0.01 μg to 100 g per kg of body weight, once or more daily, to once every 20 years.

Thus, in the context of this invention, by "therapeutically effective amount" is meant the amount of the compound which is required to have a therapeutic effect on the treated mammal. This amount, which will be apparent to the skilled artisan, will depend upon the type of mammal, the age and weight of the mammal, the type of disease to be treated, perhaps even the gender of the mammal, and other factors which are routinely taken into consideration when treating a mammal

with a disease. A therapeutic effect is assessed in the mammal by measuring the effect of the compound on the disease state in the animal. For example, if the disease to be treated is an inflammatory disease, symptomatic measurements (redness, swelling, or in the case of airway, penh (a measurement of pulmonary airflow). Cytokine release is another marker for inflammation which is routinely measured.

The following examples illustrate the present invention and are not intended to limit the same.

EXAMPLES

Example 1: Synthesis of Oligonucleotides

Unmodified oligodeoxynucleotides are synthesized on an automated DNA synthesizer (Applied Biosystems model 380B) using standard phosphoramidite chemistry with oxidation by iodine. ß-cyanoethyldiisopropyl-phosphoramidites were purchased from Applied Biosystems (Foster City, CA). For phosphorothioate oligonucleotides, the standard oxidation bottle was replaced by a 0.2 M solution of ^{3}H-1,2-benzodithiole-3-one 1,1-dioxide in acetonitrile for the stepwise thiation of the phosphite linkages. The thiation cycle wait step was increased to 68 seconds and was followed by the capping step.

2'-methoxy oligonucleotides are synthesized using 2'-methoxy ß-cyanoethyldiisopropyl-phosphoramidites (Chemgenes, Needham, MA) and the standard cycle for unmodified oligonucleotides, except the wait step after pulse delivery of tetrazole and base was increased to 360 seconds. Other 2'-alkoxy oligonucleotides were synthesized by a modification of this method, using appropriate 2'-modified amidites such as those available from Glen Research, Inc., Sterling, VA.

2'-fluoro oligonucleotides are synthesized as described in Kawasaki et al., *J. Med. Chem.*, *36*, 831 (1993). Briefly, the protected nucleoside N^{6}-benzoyl-2'-deoxy-2'-

fluoroadenosine is synthesized utilizing commercially available 9-ß-D-arabinofuranosyladenine as starting material and by modifying literature procedures whereby the 2'-α-fluoro atom is introduced by a S_N2-displacement of a 2'-ß-O-trifyl group. Thus N^6-benzoyl-9-ß-D-arabinofuranosyladenine is selectively protected in moderate yield as the 3',5'-ditetrahydropyranyl (THP) intermediate. Deprotection of the THP and N^6-benzoyl groups is accomplished using standard methodologies and standard methods are used to obtain the 5'-dimethoxytrityl- (DMT) and 5'-DMT-3'-phosphoramidite intermediates.

The synthesis of 2'-deoxy-2'-fluoroguanosine is accomplished using tetraisopropyldisiloxanyl (TPDS) protected 9-ß-D-arabinofuranosylguanine as starting material, and conversion to the intermediate diisobutyryl-arabinofuranosylguanosine. Deprotection of the TPDS group is followed by protection of the hydroxyl group with THP to give diisobutyryl di-THP protected arabinofuranosylguanine. Selective O-deacylation and triflation is followed by treatment of the crude product with fluoride, then deprotection of the THP groups. Standard methodologies are used to obtain the 5'-DMT- and 5'-DMT-3'-phosphoramidites.

Synthesis of 2'-deoxy-2'-fluorouridine is accomplished by the modification of a known procedure in which 2, 2'-anhydro-1-ß-D-arabinofuranosyluracil is treated with 70% hydrogen fluoride-pyridine. Standard procedures are used to obtain the 5'-DMT and 5'-DMT-3'phosphoramidites.

2'-deoxy-2'-fluorocytidine is synthesized via amination of 2'-deoxy-2'-fluorouridine, followed by selective protection to give N^4-benzoyl-2'-deoxy-2'-fluorocytidine. Standard procedures are used to obtain the 5'-DMT and 5'-DMT-3'phosphoramidites.

2'-(2-methoxyethyl)-modified amidites were synthesized according to Martin, P., *Helv. Chim. Acta*, 78,486 (1995). For

ease of synthesis, the last nucleotide was a deoxynucleotide. 2'-O-$CH_2CH_2OCH_3$-cytosines may be 5-methyl cytosines.

Synthesis of 5-Methyl cytosine monomers:

2,2'-Anhydro[1-(ß-D-arabinofuranosyl)-5-methyluridine]:

5-Methyluridine (ribosylthymine, commercially available through Yamasa, Choshi, Japan) (72.0 g, 0.279 M), diphenylcarbonate (90.0 g, 0.420 M) and sodium bicarbonate (2.0 g, 0.024 M) were added to DMF (300 mL). The mixture was heated to reflux, with stirring, allowing the evolved carbon dioxide gas to be released in a controlled manner. After 1 hour, the slightly darkened solution was concentrated under reduced pressure. The resulting syrup was poured into diethylether (2.5 L), with stirring. The product formed a gum. The ether was decanted and the residue was dissolved in a minimum amount of methanol (ca. 400 mL). The solution was poured into fresh ether (2.5 L) to yield a stiff gum. The ether was decanted and the gum was dried in a vacuum oven (60°C at 1 mm Hg for 24 hours) to give a solid which was crushed to a light tan powder (57 g, 85% crude yield). The material was used as is for further reactions.

2'-O-Methoxyethyl-5-methyluridine:

2,2'-Anhydro-5-methyluridine (195 g, 0.81 M), tris(2-methoxyethyl)borate (231 g, 0.98 M) and 2-methoxyethanol (1.2 L) were added to a 2 L stainless steel pressure vessel and placed in a pre-heated oil bath at 160°C. After heating for 48 hours at 155-160°C, the vessel was opened and the solution evaporated to dryness and triturated with MeOH (200 mL). The residue was suspended in hot acetone (1 L). The insoluble salts were filtered, washed with acetone (150 mL) and the filtrate evaporated. The residue (280 g) was dissolved in CH_3CN (600 mL) and evaporated. A silica gel column (3 kg) was packed in CH_2Cl_2/acetone/MeOH (20:5:3) containing 0.5% Et_3NH. The residue was dissolved in CH_2Cl_2 (250 mL) and adsorbed onto

silica (150 g) prior to loading onto the column. The product was eluted with the packing solvent to give 160 g (63%) of product.

2'-O-Methoxyethyl-5'-O-dimethoxytrityl-5-methyluridine:

2'-O-Methoxyethyl-5-methyluridine (160 g, 0.506 M) was co-evaporated with pyridine (250 mL) and the dried residue dissolved in pyridine (1.3 L). A first aliquot of dimethoxytrityl chloride (94.3 g, 0.278 M) was added and the mixture stirred at room temperature for one hour. A second aliquot of dimethoxytrityl chloride (94.3 g, 0.278 M) was added and the reaction stirred for an additional one hour. Methanol (170 mL) was then added to stop the reaction. HPLC showed the presence of approximately 70% product. The solvent was evaporated and triturated with CH_3CN (200 mL). The residue was dissolved in $CHCl_3$ (1.5 L) and extracted with 2x500 mL of saturated $NaHCO_3$ and 2x500 mL of saturated NaCl. The organic phase was dried over Na_2SO_4, filtered and evaporated. 275 g of residue was obtained. The residue was purified on a 3.5 kg silica gel column, packed and eluted with EtOAc/Hexane/Acetone (5:5:1) containing 0.5% Et_3NH. The pure fractions were evaporated to give 164 g of product. Approximately 20 g additional was obtained from the impure fractions to give a total yield of 183 g (57%).

3'-O-Acetyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methyluridine:

2'-O-Methoxyethyl-5'-O-dimethoxytrityl-5-methyluridine (106 g, 0.167 M), DMF/pyridine (750 mL of a 3:1 mixture prepared from 562 mL of DMF and 188 mL of pyridine) and acetic anhydride (24.38 mL, 0.258 M) were combined and stirred at room temperature for 24 hours. The reaction was monitored by tlc by first quenching the tlc sample with the addition of MeOH. Upon completion of the reaction, as judged by tlc, MeOH (50 mL) was added and the mixture evaporated at 35°C. The

residue was dissolved in $CHCl_3$ (800 mL) and extracted with 2x200 mL of saturated sodium bicarbonate and 2x200 mL of saturated NaCl. The water layers were back extracted with 200 mL of $CHCl_3$. The combined organics were dried with sodium sulfate and evaporated to give 122 g of residue (approx. 90% product). The residue was purified on a 3.5 kg silica gel column and eluted using EtOAc/Hexane(4:1). Pure product fractions were evaporated to yield 96 g (84%).

3'-O-Acetyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methyl-4-triazoleuridine:

A first solution was prepared by dissolving 3'-O-acetyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methyluridine (96 g, 0.144 M) in CH_3CN (700 mL) and set aside. Triethylamine (189 mL, 1.44 M) was added to a solution of triazole (90 g, 1.3 M) in CH_3CN (1 L), cooled to -5°C and stirred for 0.5 h using an overhead stirrer. $POCl_3$ was added dropwise, over a 30 minute period, to the stirred solution maintained at 0-10EC, and the resulting mixture stirred for an additional 2 hours. The first solution was added dropwise, over a 45 minute period, to the later solution. The resulting reaction mixture was stored overnight in a cold room. Salts were filtered from the reaction mixture and the solution was evaporated. The residue was dissolved in EtOAc (1 L) and the insoluble solids were removed by filtration. The filtrate was washed with 1x300 mL of $NaHCO_3$ and 2x300 mL of saturated NaCl, dried over sodium sulfate and evaporated. The residue was triturated with EtOAc to give the title compound.

2'-O-Methoxyethyl-5'-O-dimethoxytrityl-5-methylcytidine:

A solution of 3'-O-acetyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methyl-4-triazoleuridine (103 g, 0.141 M) in dioxane (500 mL) and NH_4OH (30 mL) was stirred at room temperature for 2 hours. The dioxane solution was evaporated and the residue azeotroped with MeOH (2x200 mL). The residue

was dissolved in MeOH (300 mL) and transferred to a 2 liter stainless steel pressure vessel. MeOH (400 mL) saturated with NH_3 gas was added and the vessel heated to 100°C for 2 hours (tlc showed complete conversion). The vessel contents were evaporated to dryness and the residue was dissolved in EtOAc (500 mL) and washed once with saturated NaCl (200 mL). The organics were dried over sodium sulfate and the solvent was evaporated to give 85 g (95%) of the title compound.

N^4-Benzoyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methyl-cytidine:

2'-O-Methoxyethyl-5'-O-dimethoxytrityl-5-methylcytidine (85 g, 0.134 M) was dissolved in DMF (800 mL) and benzoic anhydride (37.2 g, 0.165 M) was added with stirring. After stirring for 3 hours, tlc showed the reaction to be approximately 95% complete. The solvent was evaporated and the residue azeotroped with MeOH (200 mL). The residue was dissolved in $CHCl_3$ (700 mL) and extracted with saturated $NaHCO_3$ (2x300 mL) and saturated NaCl (2x300 mL), dried over $MgSO_4$ and evaporated to give a residue (96 g). The residue was chromatographed on a 1.5 kg silica column using EtOAc/-Hexane (1:1) containing 0.5% Et_3NH as the eluting solvent. The pure product fractions were evaporated to give 90 g (90%) of the title compound.

N^4-Benzoyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methylcytidine-3'-amidite:

N^4-Benzoyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methylcytidine (74 g, 0.10 M) was dissolved in CH_2Cl_2 (1 L). Tetrazole diisopropylamine (7.1 g) and 2-cyanoethoxy-tetra-(isopropyl)phosphite (40.5 mL, 0.123 M) were added with stirring, under a nitrogen atmosphere. The resulting mixture was stirred for 20 hours at room temperature (tlc showed the reaction to be 95% complete). The reaction mixture was extracted with saturated $NaHCO_3$ (1x300 mL) and saturated NaCl

(3x300 mL). The aqueous washes were back-extracted with CH_2Cl_2 (300 mL), and the extracts were combined, dried over $MgSO_4$ and concentrated. The residue obtained was chromatographed on a 1.5 kg silica column using EtOAc\Hexane (3:1) as the eluting solvent. The pure fractions were combined to give 90.6 g (87%) of the title compound.

5-methyl-2'-deoxycytidine (5-me-C) containing oligonucleotides were synthesized according to published methods [Sanghvi et al., *Nucl. Acids Res.*, *21*, 3197 (1993)] using commercially available phosphoramidites (Glen Research, Sterling VA or ChemGenes, Needham MA).

2'-O-(dimethylaminooxyethyl) nucleoside amidites

2'-(Dimethylaminooxyethoxy) nucleoside amidites [also known in the art as 2'-O-(dimethylaminooxyethyl) nucleoside amidites] are prepared as described in the following paragraphs. Adenosine, cytidine and guanosine nucleoside amidites are prepared similarly to the thymidine (5-methyluridine) except the exocyclic amines are protected with a benzoyl moiety in the case of adenosine and cytidine and with isobutyryl in the case of guanosine.

5'-O-tert-Butyldiphenylsilyl-O^2-2'-anhydro-5-methyluridine

O^2-2'-anhydro-5-methyluridine (Pro. Bio. Sint., Varese, Italy, 100.0g, 0.416 mmol), dimethylaminopyridine (0.66g, 0.013eq, 0.0054mmol) are dissolved in dry pyridine (500 ml) at ambient temperature under an argon atmosphere and with mechanical stirring. *tert*-Butyldiphenylchlorosilane (125.8g, 119.0mL, 1.1eq, 0.458mmol) is added in one portion. The reaction is stirred for 16 h at ambient temperature. TLC (Rf 0.22, ethyl acetate) indicates a complete reaction. The solution is concentrated under reduced pressure to a thick oil. This is partitioned between dichloromethane (1 L) and saturated sodium bicarbonate (2x1 L) and brine (1 L). The

organic layer is dried over sodium sulfate and concentrated under reduced pressure to a thick oil. The oil is dissolved in a 1:1 mixture of ethyl acetate and ethyl ether (600mL) and the solution is cooled to -10°C. The resulting crystalline product is collected by filtration, washed with ethyl ether (3x200 mL) and dried (40°C, 1mm Hg, 24 h) to 149g (74.8%) of white solid. TLC and NMR are used to check consistency with pure product.

5'-O-tert-Butyldiphenylsilyl-2'-O-(2-hydroxyethyl)-5-methyluridine

In a 2 L stainless steel, unstirred pressure reactor is added borane in tetrahydrofuran (1.0 M, 2.0 eq, 622 mL). In the fume hood and with manual stirring, ethylene glycol (350 mL, excess) is added cautiously at first until the evolution of hydrogen gas subsided. 5'-O-tert-Butyldiphenylsilyl-O^2-2'-anhydro-5-methyluridine (149 g, 0.311 mol) and sodium bicarbonate (0.074 g, 0.003 eq) are added with manual stirring. The reactor is sealed and heated in an oil bath until an internal temperature of 160 °C is reached and then maintained for 16 h (pressure < 100 psig). The reaction vessel is cooled to ambient and opened. TLC (Rf 0.67 for desired product and Rf 0.82 for ara-T side product, ethyl acetate) indicates % conversion to the product. In order to avoid additional side product formation, the reaction is stopped, concentrated under reduced pressure (10 to 1mm Hg) in a warm water bath (40-100°C) with the more extreme conditions used to remove the ethylene glycol. [Alternatively, once the low boiling solvent is gone, the remaining solution can be partitioned between ethyl acetate and water. The product will be in the organic phase.] The residue is purified by column chromatography (2kg silica gel, ethyl acetate-hexanes gradient 1:1 to 4:1). The appropriate fractions are combined, stripped and dried to product as a white crisp foam (84g, 50%), contaminated starting material (17.4g) and pure reusable

starting material 20g. TLC and NMR are used to determine consistency with pure product.

2'-O-([2-phthalimidoxy)ethyl]-5'-t-butyldiphenylsilyl-5-methyluridine

5'-O-tert-Butyldiphenylsilyl-2'-O-(2-hydroxyethyl)-5-methyluridine (20g, 36.98mmol) was mixed with triphenylphosphine (11.63g, 44.36mmol) and N-hydroxyphthalimide (7.24g, 44.36mmol). It was then dried over P_2O_5 under high vacuum for two days at 40°C. The reaction mixture was flushed with argon and dry THF (369.8mL, Aldrich, sure seal bottle) was added to get a clear solution. Diethyl-azodicarboxylate (6.98mL, 44.36mmol) was added dropwise to the reaction mixture. The rate of addition is maintained such that resulting deep red coloration is just discharged before adding the next drop. After the addition was complete, the reaction was stirred for 4 hrs. By that time TLC showed the completion of the reaction (ethylacetate:hexane, 60:40). The solvent was evaporated in vacuum. Residue obtained was placed on a flash column and eluted with ethyl acetate:hexane (60:40), to get 2'-O-([2-phthalimidoxy)ethyl]-5'-t-butyldiphenylsilyl-5-methyluridine as white foam (21.819, 86%).

5'-O-tert-butyldiphenylsilyl-2'-O-[(2-formadoximinooxy)ethyl]-5-methyluridine

2'-O-([2-phthalimidoxy)ethyl]-5'-t-butyldiphenylsilyl-5-methyluridine (3.1g, 4.5mmol) is dissolved in dry CH_2Cl_2 (4.5mL) and methylhydrazine (300mL, 4.64mmol) is added dropwise at -10°C to 0°C. After 1 hr the mixture is filtered, the filtrate is washed with ice cold CH_2Cl_2 and the combined organic phase is washed with water, brine and dried over anhydrous Na_2SO_4. The solution is concentrated to get 2'-O-(aminooxyethyl) thymidine, which is then dissolved in MeOH (67.5mL). To this formaldehyde (20% aqueous solution, w/w,

1.1eg.) is added and the mixture for 1 hr. Solvent is removed under vacuum; residue chromatographed to get 5'-O-*tert*-butyldiphenylsilyl-2'-O-[(2-formadoximinooxy) ethyl]-5-methyluridine as white foam.

5'-O-*tert*-Butyldiphenylsilyl-2'-O-[N,N-dimethylaminooxyethyl]-5-methyluridine

5'-O-*tert*-butyldiphenylsilyl-2'-O-[(2-formadoximinooxy)ethyl]-5-methyluridine (1.77g, 3.12mmol) is dissolved in a solution of 1M pyridinium p-toluenesulfonate (PPTS) in dry MeOH (30.6mL). Sodium cyanoborohydride (0.39g, 6.13mmol) is added to this solution at 10°C under inert atmosphere. The reaction mixture is stirred for 10 minutes at 10°C. After that the reaction vessel is removed from the ice bath and stirred at room temperature for 2 hr, the reaction monitored by TLC (5% MeOH in CH_2Cl_2). Aqueous $NaHCO_3$ solution (5%, 10mL) is added and extracted with ethyl acetate (2x20mL). Ethyl acetate phase is dried over anhydrous Na_2SO_4, evaporated to dryness. Residue is dissolved in a solution of 1M PPTS in MeOH (30.6mL). Formaldehyde (20% w/w, 30mL, 3.37mmol) is added and the reaction mixture is stirred at room temperature for 10 minutes. Reaction mixture cooled to 10°C in an ice bath, sodium cyanoborohydride (0.39g, 6.13mmol) is added and reaction mixture stirred at 10°C for 10 minutes. After 10 minutes, the reaction mixture is removed from the ice bath and stirred at room temperature for 2 hrs. To the reaction mixture 5% $NaHCO_3$ (25mL) solution is added and extracted with ethyl acetate (2x25mL). Ethyl acetate layer is dried over anhydrous Na_2SO_4 and evaporated to dryness. The residue obtained is purified by flash column chromatography and eluted with 5% MeOH in CH_2Cl_2 to get 5'-O-tert-butyldiphenylsilyl-2'-O-[N,N-dimethylaminooxyethyl]-5-methyluridine as a white foam (14.6g).

2'-O-(dimethylaminooxyethyl)-5-methyluridine

Triethylamine trihydrofluoride (3.91mL, 24.0mmol) is dissolved in dry THF and triethylamine (1.67mL, 12mmol, dry, kept over KOH). This mixture of triethylamine-2HF is then added to 5'-O-*tert*-butyldiphenylsilyl-2'-O-[N,N-dimethylaminooxyethyl]-5-methyluridine (1.40g, 2.4mmol) and stirred at room temperature for 24 hrs. Reaction is monitored by TLC (5% MeOH in CH_2Cl_2). Solvent is removed under vacuum and the residue placed on a flash column and eluted with 10% MeOH in CH_2Cl_2 to get 2'-O-(dimethylaminooxyethyl)-5-methyluridine (766mg).

5'-O-DMT-2'-O-(dimethylaminooxyethyl)-5-methyluridine

2'-O-(dimethylaminooxyethyl)-5-methyluridine (750mg, 2.17mmol) is dried over P_2O_5 under high vacuum overnight at 40°C. It is then co-evaporated with anhydrous pyridine (20mL). The residue obtained is dissolved in pyridine (11mL) under argon atmosphere. 4-dimethylaminopyridine (26.5mg, 2.60mmol), 4,4'-dimethoxytrityl chloride (880mg, 2.60mmol) is added to the mixture and the reaction mixture is stirred at room temperature until all of the starting material disappeared. Pyridine is removed under vacuum and the residue chromatographed and eluted with 10% MeOH in CH_2Cl_2 (containing a few drops of pyridine) to get 5'-O-DMT-2'-O-(dimethylamino-oxyethyl)-5-methyluridine (1.13g).

5'-O-DMT-2'-O-(2-N,N-dimethylaminooxyethyl)-5-methyluridine-3'-[(2-cyanoethyl)-N,N-diisopropylphosphoramidite]

5'-O-DMT-2'-O-(dimethylaminooxyethyl)-5-methyluridine (1.08g, 1.67mmol) is co-evaporated with toluene (20mL). To the residue N,N-diisopropylamine tetrazonide (0.29g, 1.67mmol) is added and dried over P_2O_5 under high vacuum overnight at 40°C. Then the reaction mixture is dissolved in anhydrous acetonitrile (8.4mL) and 2-cyanoethyl-N,N,N^1,N^1-tetraisopropylphosphoramidite (2.12mL, 6.08mmol) is added.

The reaction mixture is stirred at ambient temperature for 4 hrs under inert atmosphere. The progress of the reaction was monitored by TLC (hexane:ethyl acetate 1:1). The solvent is evaporated, then the residue is dissolved in ethyl acetate (70mL) and washed with 5% aqueous $NaHCO_3$ (40mL). Ethyl acetate layer is dried over anhydrous Na_2SO_4 and concentrated. Residue obtained is chromatographed (ethyl acetate as eluent) to get 5'-O-DMT-2'-O-(2-N,N-dimethylaminooxyethyl)-5-methyluridine-3'-[(2-cyanoethyl)-N,N-diisopropylphosphoramidite] as a foam (1.04g).

2'-(Aminooxyethoxy) nucleoside amidites

2'-(Aminooxyethoxy) nucleoside amidites [also known in the art as 2'-O-(aminooxyethyl) nucleoside amidites] are prepared as described in the following paragraphs. Adenosine, cytidine and thymidine nucleoside amidites are prepared similarly.

<u>N2-isobutyryl-6-O-diphenylcarbamoyl-2'-O-(2-ethylacetyl)-5'-O-(4,4'-dimethoxytrityl)guanosine-3'-[(2-cyanoethyl)-N,N-diisopropylphosphoramidite]</u>

The 2'-O-aminooxyethyl guanosine analog may be obtained by selective 2'-O-alkylation of diaminopurine riboside. Multigram quantities of diaminopurine riboside may be purchased from Schering AG (Berlin) to provide 2'-O-(2-ethylacetyl) diaminopurine riboside along with a minor amount of the 3'-O-isomer. 2'-O-(2-ethylacetyl) diaminopurine riboside may be resolved and converted to 2'-O-(2-ethylacetyl)guanosine by treatment with adenosine deaminase. (McGee, D. P. C., Cook, P. D., Guinosso, C. J., WO 94/02501 A1 940203.) Standard protection procedures should afford 2'-O-(2-ethylacetyl)-5'-O-(4,4'-dimethoxytrityl)guanosine and 2-N-isobutyryl-6-O-diphenylcarbamoyl-2'-O-(2-ethylacetyl)-5'-O-(4,4'-dimethoxytrityl)guanosine which may be reduced to provide 2-N-

isobutyryl-6-O-diphenylcarbamoyl-2'-O-(2-ethylacetyl)-5'-O-(4,4'-dimethoxytrityl) guanosine. As before the hydroxyl group may be displaced by N-hydroxyphthalimide via a Mitsunobu reaction, and the protected nucleoside may phosphitylated as usual to yield 2-N-isobutyryl-6-O-diphenylcarbamoyl-2'-O-(2-ethylacetyl)-5'-O-(4,4'-dimethoxytrityl)guanosine-3'-[(2-cyanoethyl)-N,N-diisopropylphosphoramidite].

Oligonucleotides having methylene(methylimino) (MMI) backbones are synthesized according to U.S. Patent No. 5,378,825, which is coassigned to the assignee of the present invention and is incorporated herein in its entirety. For ease of synthesis, various nucleoside dimers containing MMI linkages were synthesized and incorporated into oligonucleotides. Other nitrogen-containing backbones are synthesized according to WO 92/20823 which is also coassigned to the assignee of the present invention and incorporated herein in its entirety.

Oligonucleotides having amide backbones are synthesized according to De Mesmaeker et al., *Acc. Chem. Res.*, *28*, 366 (1995). The amide moiety is readily accessible by simple and well-known synthetic methods and is compatible with the conditions required for solid phase synthesis of oligonucleotides.

Oligonucleotides with morpholino backbones are synthesized according to U.S. Patent No. 5,034,506 (Summerton and Weller).

Peptide-nucleic acid (PNA) oligomers are synthesized according to P.E. Nielsen et al., *Science*, *254*, 1497 (1991).

After cleavage from the controlled pore glass column (Applied Biosystems) and deblocking in concentrated ammonium hydroxide at 55°C for 18 hours, the oligonucleotides are purified by precipitation twice out of 0.5 M NaCl with 2.5 volumes ethanol. Synthesized oligonucleotides were analyzed by polyacrylamide gel electrophoresis on denaturing gels and judged to be at least 85% full length material. The relative

amounts of phosphorothioate and phosphodiester linkages obtained in synthesis were periodically checked by ^{31}P nuclear magnetic resonance spectroscopy, and for some studies oligonucleotides were purified by HPLC, as described by Chiang et al., *J. Biol. Chem., 266,* 18162 (1991). Results obtained with HPLC-purified material were similar to those obtained with non-HPLC purified material.

RNA oligonucleotides:

In general, RNA synthesis chemistry is based on the selective incorporation of various protecting groups at strategic intermediary reactions. Although one of ordinary skill in the art will understand the use of protecting groups in organic synthesis, a useful class of protecting groups includes silyl ethers. In particular bulky silyl ethers are used to protect the 5'-hydroxyl in combination with an acid-labile orthoester protecting group on the 2'-hydroxyl. This set of protecting groups is then used with standard solid-phase synthesis technology. It is important to lastly remove the acid labile orthoester protecting group after all other synthetic steps. Moreover, the early use of the silyl protecting groups during synthesis ensures facile removal when desired, without undesired deprotection of 2' hydroxyl.

Following this procedure for the sequential protection of the 5'-hydroxyl in combination with protection of the 2'-hydroxyl by protecting groups that are differentially removed and are differentially chemically labile, RNA oligonucleotides were synthesized.

RNA oligonucleotides are synthesized in a stepwise fashion. Each nucleotide is added sequentially (3'- to 5'-direction) to a solid support-bound oligonucleotide. The first nucleoside at the 3'-end of the chain is covalently attached to a solid support. The nucleotide precursor, a ribonucleoside phosphoramidite, and activator are added, coupling the second base onto the 5'-end of the first nucleoside. The support is washed and any unreacted 5'-hydroxyl groups are capped with

acetic anhydride to yield 5'-acetyl moieties. The linkage is then oxidized to the more stable and ultimately desired P(V) linkage. At the end of the nucleotide addition cycle, the 5'-silyl group is cleaved with fluoride. The cycle is repeated for each subsequent nucleotide.

Following synthesis, the methyl protecting groups on the phosphates are cleaved in 30 minutes utilizing 1 M disodium-2-carbamoyl-2-cyanoethylene-1,1-dithiolate trihydrate (S_2Na_2) in DMF. The deprotection solution is washed from the solid support-bound oligonucleotide using water. The support is then treated with 40% methylamine in water for 10 minutes at 55 °C. This releases the RNA oligonucleotides into solution, deprotects the exocyclic amines, and modifies the 2'- groups. The oligonucleotides can be analyzed by anion exchange HPLC at this stage.

The 2'-orthoester groups are the last protecting groups to be removed. The ethylene glycol monoacetate orthoester protecting group developed by Dharmacon Research, Inc. (Lafayette, CO), is one example of a useful orthoester protecting group which, has the following important properties. It is stable to the conditions of nucleoside phosphoramidite synthesis and oligonucleotide synthesis. However, after oligonucleotide synthesis the oligonucleotide is treated with methylamine which not only cleaves the oligonucleotide from the solid support but also removes the acetyl groups from the orthoesters. The resulting 2-ethyl-hydroxyl substituents on the orthoester are less electron withdrawing than the acetylated precursor. As a result, the modified orthoester becomes more labile to acid-catalyzed hydrolysis. Specifically, the rate of cleavage is approximately 10 times faster after the acetyl groups are removed. Therefore, this orthoester possesses sufficient stability in order to be compatible with oligonucleotide synthesis and yet, when subsequently modified, permits deprotection to be carried out under relatively mild aqueous

conditions compatible with the final RNA oligonucleotide product.

Additionally, methods of RNA synthesis are well known in the art (Scaringe, S. A. Ph.D. Thesis, University of Colorado, 1996; Scaringe, S. A., et al., *J. Am. Chem. Soc.*, **1998**, *120*, 11820-11821; Matteucci, M. D. and Caruthers, M. H. *J. Am. Chem. Soc.*, **1981**, *103*, 3185-3191; Beaucage, S. L. and Caruthers, M. H. *Tetrahedron Lett.*, **1981**, *22*, 1859-1862; Dahl, B. J., et al., *Acta Chem. Scand,*. **1990**, *44*, 639-641; Reddy, M. P., et al., *Tetrahedrom Lett.*, **1994**, *25*, 4311-4314; Wincott, F. et al., *Nucleic Acids Res.*, **1995**, *23*, 2677-2684; Griffin, B. E., et al., *Tetrahedron*, **1967**, *23*, 2301-2313; Griffin, B. E., et al., *Tetrahedron*, **1967**, *23*, 2315-2331).

Example 2: Human p38α Oligonucleotide Sequences

Antisense oligonucleotides were designed to target human p38α. Target sequence data are from the p38 MAPK cDNA sequence; Genbank accession number L35253, provided herein as SEQ ID NO: 1. Oligonucleotides was synthesized as chimeric oligonucleotides ("gapmers") 20 nucleotides in length, composed of a central "gap" region consisting of eight 2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by six-nucleotide "wings." The wings are composed of 2'-methoxyethyl (2'-MOE) nucleotides. The internucleoside (backbone) linkages are phosphorothioate (P=S) throughout the oligonucleotide. All 2'-MOE cytosines were 5-methyl-cytosines. These oligonucleotide sequences are shown in Table 1.

The human Jurkat T-cell line (American Type Culture Collection, Manassas, VA) was maintained in RPMI 1640 growth media supplemented with 10% fetal bovine serum (FBS; Hyclone, Logan, UT). HUVEC cells (Clonetics, San Diego, CA) were

cultivated in endothelial basal media supplemented with 10% FBS (Hyclone, Logan, UT).

Jurkat cells were grown to approximately 75% confluency and resuspended in culture media at a density of 1 x 10^7 cells/ml. A total of 3.6 x 10^6 cells were employed for each treatment by combining 360 µl of cell suspension with oligonucleotide at the indicated concentrations to reach a final volume of 400 µl. Cells were then transferred to an electroporation cuvette and electroporated using an Electrocell Manipulator 600 instrument (Biotechnologies and Experimental Research, Inc.) employing 150 V, 1000 µF, at 13 Ω. Electroporated cells were then transferred to conical tubes containing 5 ml of culture media, mixed by inversion, and plated onto 10 cm culture dishes.

HUVEC cells were allowed to reach 75% confluency prior to use. The cells were washed twice with warm (37°C) OPTI-MEM™ (Life Technologies). The cells were incubated in the presence of the appropriate culture medium, without the growth factors added, and the oligonucleotide formulated in LIPOFECTIN7 (Life Technologies), a 1:1 (w/w) liposome formulation of the cationic lipid N-[1-(2,3-dioleyloxy)propyl]-n,n,n-trimethylammonium chloride (DOTMA), and dioleoyl phosphotidylethanolamine (DOPE) in membrane filtered water. HUVEC cells were treated with 100 nM oligonucleotide in 10 µg/ml LIPOFECTIN7. Treatment was for four hours.

Total mRNA was isolated using the RNEASY7 Mini Kit (Qiagen, Valencia, CA; similar kits from other manufacturers may also be used), separated on a 1% agarose gel, transferred to HYBOND™-N+ membrane (Amersham Pharmacia Biotech, Piscataway, NJ), a positively charged nylon membrane, and probed. p38 MAPK probes were made using the Prime-A-Gene7 kit (Promega Corporation, Madison, WI), a random primer labeling kit, using mouse p38α or p38β cDNA as a template. A

glyceraldehyde 3-phosphate dehydrogenase (G3PDH) probe was purchased from Clontech (Palo Alto, CA), Catalog Number 9805-1. The fragments were purified from low-melting temperature agarose, as described in Maniatis, T., *et al.*, *Molecular Cloning: A Laboratory Manual*, **1989**. The G3PDH probe was labeled with REDIVUE™ ^{32}P-dCTP (Amersham Pharmacia Biotech, Piscataway, NJ) and Strip-EZ labelling kit (Ambion, Austin, TX). mRNA was quantitated by a PhosphoImager (Molecular Dynamics, Sunnyvale, CA).

TABLE 1:

Nucleotide Sequences of Human p38α Chimeric (deoxy gapped) Phosphorothioate Oligonucleotides

ISIS NO.	NUCLEOTIDE SEQUENCE[1] (5' -> 3')	SEQ ID NO:	TARGET GENE NUCLEOTIDE CO-ORDINATES[2]	GENE TARGET REGION
16486	**AAGACC**GGGCCCGG**AATTCC**	3	0001-0020	5'-UTR
16487	**GTGGAG**GCCAGTCC**CCGGGA**	4	0044-0063	5'-UTR
16488	**TGGCAG**CAAAGTGC**TGCTGG**	5	0087-0106	5'-UTR
16489	**CAGAGA**GCCTCCTG**GGAGGG**	6	0136-0155	5'-UTR
16490	**TGTGCC**GAATCTCG**GCCTCT**	7	0160-0179	5'-UTR
16491	**GGTCTC**GGGCGACC**TCTCCT**	8	0201-0220	5'-UTR
16492	**CAGCCG**CGGGACCA**GCGGCG**	9	0250-0269	5'-UTR
16493	**CATTTT**CCAGCGGC**AGCCGC**	10	0278-0297	AUG
16494	**TCCTGA**GACATTTT**CCAGCG**	11	0286-0305	AUG
16495	**CTGCCG**GTAGAACG**TGGGCC**	12	0308-0327	coding
16496	**GTAAGC**TTCTGACA**TTTCAC**	13	0643-0662	coding

16497	**TTTAGG**TCCCTGTG**AATTAT**	14	0798-0817	coding
16498	**ATGTTC**TTCCAGTC**AACAGC**	15	0939-0958	coding
16499	**TAAGGA**GGTCCCTG**CTTTCA**	16	1189-1208	coding
16500	**AACCAG**GTGCTCAG**GACTCC**	17	1368-1387	stop
16501	**GAAGTG**GGATCAAC**AGAACA**	18	1390-1409	3'-UTR
16502	**TGAAAA**GGCCTTCC**CCTCAC**	19	1413-1432	3'-UTR
16503	**AGGCAC**TTGAATAA**TATTTG**	20	1444-1463	3'-UTR
16504	**CTTCCA**CCATGGAG**GAAATC**	21	1475-1494	3'-UTR
16505	**ACACAT**GCACACAC**ACTAAC**	22	1520-1539	3'-UTR

[1] Emboldened residues, 2'-methoxyethoxy- residues (others are 2'-deoxy-) including "**C**" residues, 5-methyl-cytosines; all linkages are phosphorothioate linkages.

[2] Co-ordinates from Genbank Accession No. L35253, locus name "HUMMAPKNS", SEQ ID NO. 1.

For an initial screen of human p38α antisense oligonucleotides, Jurkat cells were electroporated with 10 μM oligonucleotide. mRNA was measured by Northern blot. Results are shown in Table 2. Oligonucleotides 16496 (SEQ ID NO. 13), 16500 (SEQ ID NO. 17) and 16503 (SEQ ID NO. 20) gave 35% or greater inhibition of p38α mRNA.

TABLE 2

Inhibition of Human p38α mRNA expression in Jurkat Cells by Chimeric (deoxy gapped) Phosphorothioate Oligonucleotides

ISIS No:	SEQ ID NO:	GENE TARGET REGION	% mRNA EXPRESSION	% mRNA INHIBITION
control	---	---	100%	0%
16486	3	5'-UTR	212%	---
16487	4	5'-UTR	171%	---
16488	5	5'-UTR	157%	---
16489	6	5'-UTR	149%	---
16490	7	5'-UTR	152%	---
16491	8	5'-UTR	148%	---
16492	9	5'-UTR	125%	---
16493	10	AUG	101%	---
16494	11	AUG	72%	28%
16495	12	coding	72%	28%
16496	13	coding	61%	39%
16497	14	coding	104%	---
16498	15	coding	88%	12%
16499	16	coding	74%	26%
16500	17	stop	63%	37%
16501	18	3'-UTR	77%	23%

ISIS No:	SEQ ID NO:	GENE TARGET REGION	% mRNA EXPRESSION	% mRNA INHIBITION
16502	19	3'-UTR	79%	21%
16503	20	3'-UTR	65%	35%
16504	21	3'-UTR	72%	28%
16505	22	3'-UTR	93%	7%

The most active human p38α oligonucleotides were chosen for dose response studies. Oligonucleotide 16490 (SEQ ID NO. 7) which showed no inhibition in the initial screen was included as a negative control. Jurkat cells were grown and treated as described above except the concentration of oligonucleotide was varied as indicated in Table 3. Results are shown in Table 3. Each of the active oligonucleotides showed a dose response effect with IC_{50}s around 10 nM. Maximum inhibition was approximately 70% with 16500 (SEQ ID NO. 17). The most active oligonucleotides were also tested for their ability to inhibit p38β. None of these oligonucleotides significantly reduced p38β mRNA expression.

TABLE 3

Dose Response of p38α mRNA in Jurkat cells to human p38α Chimeric (deoxy gapped) Phosphorothioate Oligonucleotides

ISIS #	SEQ ID NO:	ASO Gene Target	Dose	% mRNA Expression	% mRNA Inhibition
control	---	---	---	100%	0%
16496	13	coding	2.5 nM	94%	6%
"	"	"	5 nM	74%	26%
"	"	"	10 nM	47%	53%

"	"	"	20 nM	41%	59%
16500	17	stop	2.5 nM	82%	18%
"	"	"	5 nM	71%	29%
"	"	"	10 nM	49%	51%
"	"	"	20 nM	31%	69%
16503	20	3'-UTR	2.5 nM	74%	26%
"	"	"	5 nM	61%	39%
"	"	"	10 nM	53%	47%
"	"	"	20 nM	41%	59%
16490	7	5'-UTR	2.5 nM	112%	---
"	"	"	5 nM	109%	---
"	"	"	10 nM	104%	---
"	"	"	20 nM	97%	3%

Example 3: Human p38β Oligonucleotide Sequences

Antisense oligonucleotides were designed to target human p38β. Target sequence data are from the p38β MAPK cDNA sequence; Genbank accession number U53442, provided herein as SEQ ID NO: 23. Oligonucleotides was synthesized as chimeric oligonucleotides ("gapmers") 20 nucleotides in length, composed of a central "gap" region consisting of ten 2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by five-nucleotide "wings." The wings are composed of 2'-methoxyethyl (2'-MOE) nucleotides. The internucleoside (backbone) linkages are phosphorothioate (P=S) throughout the oligonucleotide. All 2'-MOE cytosines were 5-methyl-cytosines. These oligonucleotide sequences are shown in Table 4.

TABLE 4:

Nucleotide Sequences of Human p38β Phosphorothioate Oligonucleotides

ISIS NO.	NUCLEOTIDE SEQUENCE[1] (5' -> 3')	SEQ ID NO:	TARGET GENE NUCLEOTIDE CO-ORDINATES[2]	GENE TARGET REGION
17891	CGACATGTCCGGAGCAGAAT	25	0006-0025	AUG
17892	TTCAGCTCCTGCCGGTAGAA	26	0041-0060	coding
17893	TGCGGCACCTCCCACACGGT	27	0065-0084	coding
17894	CCGAACAGACGGAGCCGTAT	28	0121-0140	coding
17895	GTGCTTCAGGTGCTTGAGCA	29	0240-0259	coding
17896	GCGTGAAGACGTCCAGAAGC	30	0274-0293	coding
17897	ACTTGACGATGTTGTTCAGG	31	0355-0374	coding
17898	AACGTGCTCGTCAAGTGCCA	32	0405-0424	coding
17899	ATCCTGAGCTCACAGTCCTC	33	0521-0540	coding
17900	ACTGTTTGGTTGTAATGCAT	34	0635-0654	coding
17901	ATGATGCGCTTCAGCTGGTC	35	0731-0750	coding
17902	GCCAGTGCCTCAGCTGCACT	36	0935-0954	coding
17903	AACGCTCTCATCATATGGCT	37	1005-1024	coding
17904	CAGCACCTCACTGCTCAATC	38	1126-1145	stop
17905	TCTGTGACCATAGGAGTGTG	39	1228-1247	3'-UTR
17906	ACACATGTTTGTGCATGCAT	40	1294-1313	3'-UTR
17907	CCTACACATGGCAAGCACAT	41	1318-1337	3'-UTR
17908	TCCAGGCTGAGCAGCTCTAA	42	1581-1600	3'-UTR

17909	**AGTGC**ACGCTCATC**CACACG**	43	1753-1772	3'-UTR
17910	**CTTGC**CAGATATGG**CTGCTG**	44	1836-1855	3'-UTR

[1] Emboldened residues, 2'-methoxyethoxy- residues (others are 2'-deoxy-) including "C" residues, 5-methyl-cytosines; all linkages are phosphorothioate linkages.

[2] Co-ordinates from Genbank Accession No. U53442, locus name "HSU53442", SEQ ID NO. 23.

For an initial screen of human p38β antisense oligonucleotides, HUVEC cells were cultured and treated as described in Example 2. mRNA was measured by Northern blot as described in Example 2. Results are shown in Table 5. Every oligonucleotide tested gave at least 50% inhibition. Oligonucleotides 17892 (SEQ ID NO. 26), 17893 (SEQ ID NO. 27), 17894 (SEQ ID NO. 28), 17899 (SEQ ID NO. 33), 17901 (SEQ ID NO. 35), 17903 (SEQ ID NO. 37), 17904 (SEQ ID NO. 38), 17905 (SEQ ID NO. 39), 17907 (SEQ ID NO. 41), 17908 (SEQ ID NO. 42), and 17909 (SEQ ID NO. 43) gave greater than approximately 85% inhibition and are preferred.

TABLE 5

Inhibition of Human p38β mRNA expression in Huvec Cells by Chimeric (deoxy gapped) Phosphorothioate Oligonucleotides

ISIS No:	SEQ ID NO:	GENE TARGET REGION	% mRNA EXPRESSION	% mRNA INHIBITION
control	---	---	100%	0%
17891	25	AUG	22%	78%

ISIS No:	SEQ ID NO:	GENE TARGET REGION	% mRNA EXPRESSION	% mRNA INHIBITION
17892	26	coding	10%	90%
17893	27	coding	4%	96%
17894	28	coding	13%	87%
17895	29	coding	25%	75%
17896	30	coding	24%	76%
17897	31	coding	25%	75%
17898	32	coding	49%	51%
17899	33	coding	5%	95%
17900	34	coding	40%	60%
17901	35	coding	15%	85%
17902	36	coding	49%	51%
17903	37	coding	11%	89%
17904	38	stop	9%	91%
17905	39	3'-UTR	14%	86%
17906	40	3'-UTR	22%	78%
17907	41	3'-UTR	8%	92%
17908	42	3'-UTR	17%	83%
17909	43	3'-UTR	13%	87%
17910	44	3'-UTR	26%	74%

Oligonucleotides 17893 (SEQ ID NO. 27), 17899 (SEQ ID NO. 33), 17904 (SEQ ID NO. 38), and 17907 (SEQ ID NO. 41) were chosen for dose response studies. HUVEC cells were cultured

and treated as described in Example 2 except that the oligonucleotide concentration was varied as shown in Table 6. The Lipofectin7/Oligo ratio was maintained at 3µg Lipofectin7/100nM oligo, per ml. mRNA was measured by Northern blot as described in Example 2.

Results are shown in Table 6. Each oligonucleotide tested had an IC_{50} of less than 10 nM. The effect of these oligonucleotides on human p38α was also determined. Only oligonucleotide 17893 (SEQ ID NO. 27) showed an effect on p38α mRNA expression. The IC_{50} of this oligonucleotide was approximately 4 fold higher for p38α compared to p38β.

TABLE 6

Dose Response of p38β in Huvec cells to human p38β Chimeric (deoxy gapped) Phosphorothioate Oligonucleotides

ISIS #	SEQ ID NO:	ASO Gene Target	Dose	% mRNA Expression	% mRNA Inhibition
control	---	---	---	100%	0%
17893	27	coding	10 nM	37%	63%
"	"	"	25 nM	18%	82%
"	"	"	50 nM	16%	84%
"	"	"	100 nM	19%	81%
17899	33	coding	10 nM	37%	63%
"	"	"	25 nM	23%	77%
"	"	"	50 nM	18%	82%
"	"	"	100 nM	21%	79%
17904	38	stop	10 nM	31%	69%
"	"	"	25 nM	21%	79%
"	"	"	50 nM	17%	83%

"	"	"	100 nM	19%	81%
17907	41	3'-UTR	10 nM	37%	63%
"	"	"	25 nM	22%	78%
"	"	"	50 nM	18%	72%
"	"	"	100 nM	18%	72%

Example 4: Rat p38α Oligonucleotide Sequences

Antisense oligonucleotides were designed to target rat p38α. Target sequence data are from the p38 MAPK cDNA sequence; Genbank accession number U73142, provided herein as SEQ ID NO: 45. Oligonucleotides was synthesized as chimeric oligonucleotides ("gapmers") 20 nucleotides in length, composed of a central "gap" region consisting of ten 2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by five-nucleotide "wings." The wings are composed of 2'-methoxyethyl (2'-MOE) nucleotides. The internucleoside (backbone) linkages in the wings are phosphodiester (P=O). Internucleoside linkages in the central gap are phosphorothioate (P=S). All 2'-MOE cytosines and 2'-OH cytosines were 5-methyl-cytosines. These oligonucleotide sequences are shown in Table 7.

bEND.3, a mouse endothelial cell line (gift of Dr. Werner Risau; see Montesano *et al.*, *Cell*, 1990, *62*, 435, and Stepkowski *et al.*, *J. Immunol.*, 1994, *153*, 5336) were grown in high-glucose DMEM (Life Technologies, Gaithersburg, MD) medium containing 10% fetal bovine serum (FBS) and 1% Penicillin/Streptomycinin. Cells were plated at approximately 2 x 10^5 cells per 100 mm dish. Within 48 hours of plating, the cells were washed with phosphate-buffered saline (Life Technologies). Then, Opti-MEM7 medium containing 3 μg/mL LIPOFECTIN^7 and an appropriate amount of oligonucleotide were added to the cells. As a control, cells were treated with

LIPOFECTIN[7] without oligonucleotide under the same conditions and for the same times as the oligonucleotide-treated samples.

After 4 hours at 37°C, the medium was replaced with high glucose DMEM medium containing 10% FBS and 1% Penicillin/Streptomycinin. The cells were typically allowed to recover overnight (about 18 to 24 hours) before RNA and/or protein assays were performed as described in Example 2. The p38α, p38β and G3PDH probes used were identical to those described in Example 2.

TABLE 7:

Nucleotide Sequences of Rat p38α Phosphorothioate Oligonucleotides

ISIS NO.	NUCLEOTIDE SEQUENCE[1] (5' -> 3')	SEQ ID NO	TARGET GENE NUCLEOTIDE CO-ORDINATES[2]	GENE TARGET REGION
21844	CoToGoCoGsAsCsAsTsTsTsTsCsCsAsGoCoGoGoC	47	0001-0020	AUG
21845	GoGoToAoAsGsCsTsTsCsTsGsAsCsAsCoToToCoA	48	0361-0380	coding
21846	GoGoCoCoAsGsAsGsAsCsTsGsAsAsTsGoToAoGoT	49	0781-0800	coding
21871	CoAoToCoAsTsCsAsGsGsGsTsCsGsTsGoGoToAoC	50	0941-0960	coding
21872	GoGoCoAoCsAsAsAsGsCsTsAsAsTsGsAoCoToToC	51	1041-1060	coding
21873	AoGoGoToGsCsTsCsAsGsGsAsCsTsCsCoAoToToT	52	1081-1100	stop
21874	GoGoAoToGsGsAsCsAsGsAsAsCsAsGsAoAoGoCoA	53	1101-1120	3'-UTR
21875	GoAoGoCoAsGsGsCsAsGsAsCsTsGsCsCoAoAoGoG	54	1321-1340	3'-UTR
21876	AoGoGoCoTsAsGsAsGsCsCsCsAsGsGsAoGoCoCoA	55	1561-1580	3'-UTR

21877	GoAoGoCoCsTsGsTsGsCsCsTsGsGsCsAoCoToGoG	56	1861-1880	3'-UTR
21878	ToGoCoAoCsCsAsCsAsCsAsGsCsAsCsCsToGoGoAoG	57	2081-2100	3'-UTR
21879	GoGoCoToAsCsCsAsTsGsAsGsTsGsAsGoAoAoGoA	58	2221-2240	3'-UTR
21880	GoToCoCoCsTsGsCsAsCsTsGsAsTsAsGoAoGoAoA	59	2701-2720	3'-UTR
21881	ToCoToToCsCsAsAsTsGsGsAsGsAsAoCoToGoG	60	3001-3020	3'-UTR

[1] Emboldened residues, 2'-methoxyethoxy- residues (others are 2'-deoxy-); 2'-MOE cytosines and 2'-deoxy cytosine residues are 5-methyl-cytosines; "s" linkages are phosphorothioate linkages; "o" linkages are phosphodiester linkages.

[2] Co-ordinates from Genbank Accession No. U73142, locus name "RNU73142", SEQ ID NO. 45.

Rat p38α antisense oligonucleotides were screened in bEND.3 cells for inhibition of p38α and p38β mRNA expression. The concentration of oligonucleotide used was 100 nM. Results are shown in Table 8. Oligonucleotides 21844 (SEQ ID NO. 47), 21845 (SEQ ID NO. 48), 21872 (SEQ ID NO. 51), 21873 (SEQ ID NO. 52), 21875 (SEQ ID NO. 54), and 21876 (SEQ ID NO. 55) showed greater than approximately 70% inhibition of p38α mRNA with minimal effects on p38β mRNA levels. Oligonucleotide 21871 (SEQ ID NO. 50) inhibited both p38α and p38β levels greater than 70%.

TABLE 8

Inhibition of Mouse p38 mRNA expression in bEND.3 Cells by Chimeric (deoxy gapped) Mixed Backbone p38α Antisense Oligonucleotides

ISIS No:	SEQ ID NO:	GENE TARGET REGION	% p38α mRNA INHIBITION	% p38β mRNA INHIBITION
control	---	---	0%	0%
21844	47	AUG	81%	20%
21845	48	coding	75%	25%
21871	50	coding	90%	71%

ISIS No:	SEQ ID NO:	GENE TARGET REGION	% p38α mRNA INHIBITION	% p38β mRNA INHIBITION
21872	51	coding	87%	23%
21873	52	stop	90%	3%
21874	53	3'-UTR	38%	21%
21875	54	3'-UTR	77%	---
21876	55	3'-UTR	69%	---
21877	56	3'-UTR	55%	13%
21878	57	3'-UTR	25%	10%
21879	58	3'-UTR	---	---
21881	60	3'-UTR	---	---

Several of the most active oligonucleotides were selected for dose response studies. bEND.3 cells were cultured and treated as described above, except that the concentration of oligonucleotide was varied as noted in Table 9. Results are shown in Table 9.

TABLE 9

Dose Response of bEND.3 cells to rat p38β Chimeric (deoxy gapped) Phosphorothioate Oligonucleotides

ISIS #	SEQ ID NO:	ASO Gene Target	Dose	% p38α mRNA Inhibition	% p38β mRNA Inhibition
control	---	---	---	100%	0%
21844	47	AUG	1 nM	---	---

"	"	"	5 nM	---	---
"	"	"	25 nM	36%	8%
"	"	"	100 nM	80%	5%
21871	50	coding	1 nM	1%	---
"	"	"	5 nM	23%	4%
"	"	"	25 nM	34%	24%
"	"	"	100 nM	89%	56%
21872	51	stop	1 nM	---	---
"	"	"	5 nM	---	---
"	"	"	25 nM	35%	---
"	"	"	100 nM	76%	1%
21873	52	stop	1 nM	---	53%
"	"	"	5 nM	---	31%
"	"	"	25 nM	54%	28%
"	"	"	100 nM	92%	25%
21875	54	3'-UTR	1 nM	---	11%
"	"	"	5 nM	---	16%
"	"	"	25 nM	33%	2%
"	"	"	100 nM	72%	4%

Example 5: Mouse p38β Oligonucleotide Sequences

Antisense oligonucleotides were designed to target mouse p38β. Target sequence data are from a mouse EST sequence; Genbank accession number AI119044, provided herein as SEQ ID NO: 61. Oligonucleotides was synthesized as chimeric oligonucleotides ("gapmers") 20 nucleotides in length, composed of a central "gap" region consisting of ten

2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by five-nucleotide "wings." The wings are composed of 2'-methoxyethyl (2'-MOE) nucleotides. The internucleoside (backbone) linkages in the wings are phosphodiester (P=O). Internucleoside linkages in the central gap are phosphorothioate (P=S). All 2'-MOE cytosines and 2'-OH cytosines were 5-methyl-cytosines. These oligonucleotide sequences are shown in Table 10.

TABLE 10:

Nucleotide Sequences of Mouse p38β

Chimeric (deoxy gapped) Phosphorothioate Oligonucleotides

ISIS NO.	NUCLEOTIDE SEQUENCE[1] (5' -> 3')	SEQ ID NO:	TARGET GENE NUCLEOTIDE CO-ORDINATES[2]
100800	CoAoCoAoGsAsAsGsCsAsGsCsTsGsGsAoGoCoGoA	63	0051-0070
100801	ToGoCoGoGsCsAsCsCsTsCsCsCsAsTsAoCoToGoT	64	0119-0138
100802	CoCoCoToGsCsAsGsCsCsGsCsTsGsCsGoGoCoAoC	65	0131-0150
100803	GoCoAoGoAsCsTsGsAsGsCsCsGsTsAsGoGoCoGoC	66	0171-0190
100804	ToToAoCoAsGsCsCsAsCsCsTsTsCsTsGoGoCoGoC	67	0211-0230
100805	GoToAoToGsTsCsCsTsCsCsTsCsGsCsGoToGoGoA	68	0261-0280
100806	AoToGoGoAsTsGsTsGsGsCsCsGsGsCsGoToGoAoA	69	0341-0360
100807	GoAoAoToTsGsAsAsCsAsTsGsCsTsCsAoToCoGoC	70	0441-0460
100808	AoCoAoToTsGsCsTsGsGsGsCsTsTsCsAoGoGoToC	71	0521-0540
100809	AoToCoCoToTsCsAsGsCsTsCsGsCsAsGsToCoCoToC	72	0551-0570
100810	ToAoCoCoCoAsCsCsGsTsGsTsGsGsCsCsAoCoAoToA	73	0617-0636

100811	**CoAoGoToTsTsAsGsCsAsTsGsAsTsCsToCoToGoG**	74	0644-0663
100812	**CoAoGoGoCsCsAsCsAsGsAsCsCsAsGsAoToGoToC**	75	0686-0705
100813	**CoCoToToCsCsAsGsCsAsGsTsTsCsAsAoGoCoCoA**	76	0711-0730
101123	**CoAoGoCoAsCsCsAsTsGsGsAsCsGsCsGoGoAoAoC**	77	21871 mismatch

[1] Emboldened residues, 2'-methoxyethoxy- residues (others are 2'-deoxy-), including 2'-MOE and 2'-deoxy residues, 5-methyl-cytosines; "s" linkages are phosphorothioate linkages, "o" linkages are phosphodiester.

[2] Co-ordinates from Genbank Accession No. AI119044, locus name "AI119044", SEQ ID NO. 61.

Mouse p38β antisense sequences were screened in bEND.3 cells as described in Example 4. Results are shown in Table 11.

Oligonucleotides 100800 (SEQ ID NO. 63), 100801 (SEQ ID NO. 64), 100803 (SEQ ID NO. 66), 100804 (SEQ ID NO. 67), 100805 (SEQ ID NO. 68), 100807 (SEQ ID NO. 70), 100808 (SEQ ID NO. 71), 100809 (SEQ ID NO. 72), 100810 (SEQ ID NO. 73), 100811 (SEQ ID NO.74), and 100813 (SEQ ID NO. 76) resulted in at least 50% inhibition of p38β mRNA expression. Oligonucleotides 100801 (SEQ ID NO.64), 100803 (SEQ ID NO. 66), 100804 (SEQ ID NO. 67), 100805 (SEQ ID NO. 68), 100809 (SEQ ID NO. 72), and 100810 (SEQ ID NO. 73) resulted in at least 70% inhibition and are preferred. Oligonucleotides 100801 (SEQ ID NO. 64), 100805 (SEQ ID NO. 68), and 100811 (SEQ ID NO. 74) resulted in significant inhibition of p38α mRNA expression in addition to their effects on p38β.

TABLE 11

Inhibition of Mouse p38 mRNA expression in bEND.3 Cells by Chimeric (deoxy gapped) Mixed Backbone p38β Antisense Oligonucleotides

ISIS No:	SEQ ID NO:	% p38β mRNA INHIBITION	% p38α mRNA INHIBITION
control	---	0%	0%
100800	63	51%	---
100801	64	74%	31%
100802	65	35%	---
100803	66	74%	18%
100804	67	85%	18%
100805	68	78%	58%
100806	69	22%	3%
100807	70	64%	---
100808	71	53%	13%
100809	72	84%	14%
100810	73	72%	1%
100811	74	60%	43%
100812	75	36%	17%
100813	76	54%	---

Example 6: Effect of p38 MAPK Antisense Oligonucleotides on IL-6 Secretion

p38 MAPK antisense oligonucleotides were tested for their ability to reduce IL-6 secretion. bEND.3 cells were cultured and treated as described in Example 4 except that 48

hours after oligonucleotide treatment, cells were stimulated for 6 hours with 1 ng/mL recombinant mouse IL-1 (R&D Systems, Minneapolis, MN). IL-6 was measured in the medium using an IL-6 ELISA kit (Endogen Inc., Woburn, MA).

Results are shown in Table 12. Oligonucleotides targeting a specific p38 MAPK isoform were effective in reducing IL-6 secretion greater than approximately 50%.

Table 12

Effect of p38 Antisense Oligonucleotides on IL-6 secretion

ISIS No:	SEQ ID NO:	GENE TARGET	DOSE (μM)	%IL-6 INHIBITION
control	---	---		0%
21873	52	p38α	100	49%
100804	67	p38β	100	57%
21871	50	p38α and p38β	200	23%

Example 7: Activity of p38α Antisense Oligonucleotides in Rat Cardiomyocytes

Rat p38α antisense oligonucleotides were screened in Rat A-10 cells. A-10 cells (American Type Culture Collection, Manassas, VA) were grown in high-glucose DMEM (Life Technologies, Gaithersburg, MD) medium containing 10% fetal calf serum (FCS). Cells were treated with oligonucleotide as described in Example 2. Oligonucleotide concentration was 200 nM. mRNA was isolated 24 hours after time zero and quantitated by Northern blot as described in Example 2.

Results are shown in Table 13. Oligonucleotides 21845 (SEQ ID NO. 48), 21846 (SEQ ID NO. 49), 21871 (SEQ ID NO. 50), 21872 (SEQ ID NO. 51), 21873 (SEQ ID NO. 52), 21874 (SEQ ID NO. 53), 21875 (SEQ ID NO. 54), 21877 (SEQ ID NO. 56), 21878

(SEQ ID NO. 57), 21879 (SEQ ID NO. 58), and 21881 (SEQ ID NO. 60) inhibited p38α mRNA expression by 65% or greater in this assay. Oligonucleotides 21846 (SEQ ID NO. 49), 21871 (SEQ ID NO. 50), 21872 (SEQ ID NO. 51), 21877 (SEQ ID NO. 56), and 21879 (SEQ ID NO. 58) inhibited p38α mRNA expression by greater than 85% and are preferred.

TABLE 13

Inhibition of Rat p38α mRNA expression in A-10 Cells by Chimeric (deoxy gapped) Mixed Backbone p38α Antisense Oligonucleotides

ISIS No:	SEQ ID NO:	GENE TARGET REGION	% p38α mRNA EXPRESSION	% p38α mRNA INHIBITION
control	---	---	100%	0%
21844	47	AUG	75%	25%
21845	48	coding	25%	75%
21846	49	coding	8%	92%
21871	50	coding	12%	88%
21872	51	coding	13%	87%
21873	52	stop	19%	81%
21874	53	3'-UTR	22%	78%
21875	54	3'-UTR	26%	74%
21876	55	3'-UTR	61%	39%
21877	56	3'-UTR	12%	88%
21878	57	3'-UTR	35%	65%
21879	58	3'-UTR	11%	89%
21881	60	3'-UTR	31%	69%

The most active oligonucleotide in this screen (SEQ ID NO. 49) was used in rat cardiac myocytes prepared from neonatal rats (Zechner, D., et. al., *J. Cell Biol.*, **1997**, *139*, 115-127). Cells were grown as described in Zechner et al. and transfected with oligonucleotide as described in Example 2. Oligonucleotide concentration was 1 μM. mRNA was isolated 24 hrs after time zero and quantitated using Northern blotting as described in Example 2. An antisense oligonucleotide targeted to JNK-2 was used as a non-specific target control.

Results are shown in Table 14. Oligonucleotide 21846 (SEQ ID NO. 49) was able to reduce p38α expression in rat cardiac myocytes by nearly 60%. The JNK-2 antisense oligonucleotide had little effect on p38α expression.

TABLE 14

Inhibition of Rat p38α mRNA expression in Rat Cardiac Myocytes by A Chimeric (deoxy gapped) Mixed Backbone p38α Antisense Oligonucleotide

ISIS No:	SEQ ID NO:	GENE TARGET REGION	% p38α mRNA EXPRESSION	% p38α mRNA INHIBITION
control	---	---	100%	0%
21846	49	coding	41%	59%

Example 8: Additional Human p38α Oligonucleotide Sequences

Additional antisense oligonucleotides were designed to target human p38α based on active rat sequences. Target sequence data are from the p38 MAPK cDNA sequence; Genbank accession number L35253, provided herein as SEQ ID NO: 1. Oligonucleotides were synthesized as chimeric oligonucleotides ("gapmers") 20 nucleotides in length, composed of a central

"gap" region consisting of ten 2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by five-nucleotide "wings." The wings are composed of 2'-methoxyethyl (2'-MOE) nucleotides. The internucleoside (backbone) linkages are phosphorothioate (P=S) throughout the oligonucleotide. All 2'-MOE cytosines and 2'-OH cytosines were 5-methyl-cytosines. These oligonucleotide sequences are shown in Table 15.

TABLE 15

Additional Nucleotide Sequences of Human p38α Chimeric (deoxy gapped) Phosphorothioate Oligonucleotides

ISIS NO.	NUCLEOTIDE SEQUENCE[1] (5' -> 3')	SEQ ID NO:	TARGET GENE NUCLEOTIDE CO-ORDINATES[2]	GENE TARGET REGION
100860	**CTGAG**ACATTTTCCA**GCGGC**	78	0284-0303	Start
100861	**ACGCT**CGGGCACCTC**CCAGA**	79	0344-0363	coding
100862	**AGCTT**CTTCACTGCC**ACACG**	80	0439-0458	coding
100863	**AATGA**TGGACTGAAA**TGGTC**	81	0464-0483	coding
100864	**TCCAA**CAGACCAATC**ACATT**	82	0538-0557	coding
100865	**TGTAA**GCTTCTGACA**TTTCA**	83	0644-0663	coding
100866	**TGAAT**GTATATACTT**TAGAC**	84	0704-0723	coding
100867	**CTCAC**AGTCTTCATT**CACAG**	85	0764-0783	coding
100868	**CACGT**AGCCTGTCATT**TCAT**	86	0824-0843	coding
100869	**CATCC**CACTGACCAA**ATATC**	87	0907-0926	coding
100870	**TATGG**TCTGTACCAG**GAAAC**	88	0960-0979	coding
100871	**AGTCA**AAGACTGAATA**TAGT**	89	1064-1083	coding

100872	**TTCTC**TTATCTGAGT**CCAAT**	90	1164-1183	coding
100873	**CATCA**TCAGGATCGT**GGTAC**	91	1224-1243	coding
100874	**TCAAA**GGACTGATCA**TAAGG**	92	1258-1277	coding
100875	**GGCAC**AAAGCTGATG**ACTTC**	93	1324-1343	coding
100876	**AGGTG**CTCAGGACTC**CATCT**	94	1364-1383	stop
100877	**GCAAC**AAGAGGCACT**TGAAT**	95	1452-1471	3'-UTR

[1] Emboldened residues, 2'-methoxyethoxy- residues (others are 2'-deoxy-) including "**C**" and "C" residues, 5-methyl-cytosines; all linkages are phosphorothioate linkages.

[2] Co-ordinates from Genbank Accession No. L35253, locus name "HUMMAPKNS", SEQ ID NO. 1.

For an initial screen of human p38α antisense oligonucleotides, T-24 cells, a human transitional cell bladder carcinoma cell line, were obtained from the American Type Culture Collection (ATCC) (Manassas, VA). T-24 cells were routinely cultured in complete McCoy's 5A basal media (Gibco/Life Technologies, Gaithersburg, MD) supplemented with 10% fetal calf serum (Gibco/Life Technologies, Gaithersburg, MD), penicillin 100 units per mL, and streptomycin 100 micrograms per mL (Gibco/Life Technologies, Gaithersburg, MD). Cells were routinely passaged by trypsinization and dilution when they reached 90% confluence. Cells were seeded into 96-well plates (Falcon-Primaria #3872) at a density of 7000 cells/well for use in RT-PCR analysis. A control oligonucleotide ISIS 118965 (TTATCCTAGCTTAGACCTAT, herein incorporated as SEQ ID NO: 96) was synthesized as chimeric oligonucleotide ("gapmer") 20 nucleotides in length, composed of a central "gap" region consisting of ten 2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by five-nucleotide "wings." The wings are

composed of 2'-methoxyethyl (2'-MOE) nucleotides. The internucleoside (backbone) linkages are phosphorothioate (P=S) throughout the oligonucleotide. All 2'-MOE cytosines and 2'-OH cytosines were 5-methyl-cytosines.

For Northern blotting or other analysis, cells may be seeded onto 100 mm or other standard tissue culture plates and treated similarly, using appropriate volumes of medium and oligonucleotide. mRNA was measured by Northern blot. Results are shown in Table 16. Oligonucleotides 100861 (SEQ ID NO. 79), 100862 (SEQ ID NO. 80), 100863 (SEQ ID NO. 81), 100866 (SEQ ID NO. 84), 100867 (SEQ ID NO. 85), 100868 (SEQ ID NO. 86), 100870 (SEQ ID NO. 88), 100871 (SEQ ID NO. 89), 100872 (SEQ ID NO. 90), 100873 (SEQ ID NO. 91), and 100874 (SEQ ID NO. 92) 100875 (SEQ ID NO. 93) and 100877 (SEQ ID NO. 95) gave greater than approximately 40% inhibition and are preferred.

TABLE 16

Inhibition of Human p38α mRNA expression in T-24 Cells by Chimeric (deoxy gapped) Phosphorothioate Oligonucleotides

ISIS No:	SEQ ID NO:	GENE TARGET REGION	% P38α mRNA EXPRESSION	% P38β mRNA EXPRESSION
100860	78	0284-0303	73%	71%
100861	79	0344-0363	60%	47%
100862	80	0439-0458	56%	45%
100863	81	0464-0483	49%	67%
100864	82	0538-0557	66%	70%
100865	83	0644-0663	64%	63%
100866	84	0704-0723	55%	65%

100867	85	0764-0783	58%	33%
100868	86	0824-0843	47%	60%
100869	87	0907-0926	61%	100%
100870	88	0960-0979	51%	No data
100871	89	1064-1083	57%	96%
100872	90	1164-1183	37%	77%
100873	91	1224-1243	34%	70%
100874	92	1258-1277	42%	76%
100875	93	1324-1343	39%	90%
100876	94	1364-1383	77%	93%
100877	95	1452-1471	47%	95%

Oligonucleotides 100872 (SEQ ID NO. 90), 100873 (SEQ ID NO. 91), 100874 (SEQ ID NO. 92), and 100875 (SEQ ID NO. 93) were chosen for dose response studies.

Results are shown in Table 17. The effect of these oligonucleotides on human p38β was also determined.

TABLE 17

Dose Response of p38α in T-24 cells to human p38α Chimeric (deoxy gapped) Phosphorothioate Oligonucleotides

ISIS #	SEQ ID NO:	ASO Gene Target	Dose	% p38α mRNA Expression	% p38β mRNA Inhibition
Control 118965	96	---	---	94%	80%
100872	90	coding	50 nM	45%	108%
"	"	"	100 nM	18%	91%

"	"	"	200 nM	17%	92%
100873	91	coding	50 nM	19%	90%
"	"	"	100 nM	12%	78%
"	"	"	200 nM	8%	44%
100874	92	coding	50 nM	47%	107%
"	"	"	100 nM	27%	101%
"	"	"	200 nM	13%	51%
100875	93	coding	50 nM	30%	105%
"	"	"	100 nM	13%	92%
"	"	"	200 nM	8%	69%

Example 9: Additional Human p38β Oligonucleotide Sequences

Additional antisense oligonucleotides were designed to target human p38β based on active rat sequences. Target sequence data are from the p38 MAPK cDNA sequence; Genbank accession number U53442, provided herein as SEQ ID NO: 23.

Oligonucleotides was synthesized as chimeric oligonucleotides ("gapmers") 20 nucleotides in length, composed of a central "gap" region consisting of ten 2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by five-nucleotide "wings." The wings are composed of 2'-methoxyethyl (2'-MOE) nucleotides. The internucleoside (backbone) linkages in the wings are phosphodiester (P=O). Internucleoside linkages in the central gap are phosphorothioate (P=S). All 2'-MOE cytosines and 2'-OH cytosines were 5-methyl-cytosines. These oligonucleotide sequences are shown in Table 18. A control oligonucleotide ISIS 118966 (GTTCGATCGGCTCGTGTCGA), herein incorporated as SEQ ID NO: 107) was synthesized as chimeric oligonucleotide ("gapmer") 20 nucleotides in length, composed of a central "gap" region consisting of ten 2'-deoxynucleotides, which is

flanked on both sides (5' and 3' directions) by five-nucleotide "wings." The wings are composed of 2'-methoxyethyl (2'-MOE) nucleotides. The internucleoside (backbone) linkages are phosphorothioate (P=S) in the gap and phosphodiester in the wings. All 2'-MOE cytosines and 2'-OH cytosines were 5-methyl-cytosines.

TABLE 18

Additional Nucleotide Sequences of Human p38β Chimeric (deoxy gapped) Mixed-Backbone Phosphorothioate Oligonucleotides

ISIS NO.	NUCLEOTIDE SEQUENCE[1] (5' -> 3')	SEQ ID NO:	TARGET GENE NUCLEOTIDE CO-ORDINATES[2]	GENE TARGET REGION
107869	**ACAGA**CGGAGCCGTA**GGCGC**	97	117-136	coding
107870	**CACCG**CCACCTTCTG**GCGCA**	98	156-175	coding
107871	**GTACG**TTCTGCGCGC**GTGGA**	99	207-226	coding
107872	**ATGGA**CGTGGCCGGC**GTGAA**	100	287-306	coding
107873	**CAGGAA**TTGAACGTG**CTCGT**	101	414-433	coding
107874	**ACGTT**GCTGGGCTTC**AGGTC**	102	491-510	coding
107875	**TACCA**GCGCGTGGCC**ACATA**	103	587-606	coding
107876	**CAGTT**GAGCATGATC**TCAGG**	104	614-633	coding
107877	**CGGAC**CAGATATCCA**CTGTT**	105	649-668	coding
107878	**TGCCC**TGGAGCAGCT**CAGCC**	106	682-701	coding

[1] Emboldened residues, 2'-methoxyethoxy- residues (others are 2'-deoxy-) including "C" and "C" residues, 5-methyl-cytosines.
[2] Co-ordinates from Genbank Accession No. U53442, SEQ ID NO. 23.

For an initial screen of human p38β antisense oligonucleotides, T-24 cells, a human transitional cell bladder carcinoma cell line, were obtained from the American Type Culture Collection (ATCC) (Manassas, VA). T-24 cells were routinely cultured in complete McCoy's 5A basal media (Gibco/Life Technologies, Gaithersburg, MD) supplemented with 10% fetal calf serum (Gibco/Life Technologies, Gaithersburg,

MD), penicillin 100 units per mL, and streptomycin 100 micrograms per mL (Gibco/Life Technologies, Gaithersburg, MD). Cells were routinely passaged by trypsinization and dilution when they reached 90% confluence. Cells were seeded into 96-well plates (Falcon-Primaria #3872) at a density of 7000 cells/well for use in RT-PCR analysis. A control oligonucleotide ISIS 118966 (TTATCCTAGCTTAGACCTAT, herein incorporated as SEQ ID NO: 106) was synthesized as chimeric oligonucleotide ("gapmer") 20 nucleotides in length, composed of a central "gap" region consisting of ten 2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by five-nucleotide "wings." The wings are composed of 2'-methoxyethyl (2'-MOE) nucleotides. The internucleoside (backbone) linkages are phosphorothioate (P=S) in the gap and phosphodiester in the wings. All 2'-MOE cytosines and 2'-OH cytosines were 5-methyl-cytosines.

For Northern blotting or other analysis, cells may be seeded onto 100 mm or other standard tissue culture plates and treated similarly, using appropriate volumes of medium and oligonucleotide. mRNA was measured by Northern blot. Results are shown in Table 19. For comparison, ISIS 17893 and ISIS 17899, both targeting human p38β (SEQ ID NO: 27) and ISIS 100802 targeting mouse p38β (SEQ ID NO: 65) described in Examples 3 and 5 above, respectively, were included in the screen.

Oligonucleotides 107869 (SEQ ID NO. 97), 107871 (SEQ ID NO. 99), 107872 (SEQ ID NO. 100), 107873 (SEQ ID NO. 101), 107878 (SEQ ID NO.106), 17893 (SEQ ID NO. 27), 17899 (SEQ ID NO. 33) and 100802 (SEQ ID NO.65, targeted to mouse p38β) gave greater than approximately 40% inhibition and are preferred.

TABLE 19

Inhibition of Human p38β mRNA expression in T-24 Cells by Chimeric (deoxy gapped) Mixed-Backbone Phosphorothioate Oligonucleotides

ISIS No:	SEQ ID NO:	GENE TARGET REGION	% p38β mRNA EXPRESSION	% p38α mRNA EXPRESSION
107869	97	Coding	60%	93%
107870	98	Coding	74%	97%
107871	99	Coding	60%	111%
107872	100	Coding	57%	123%
107873	101	Coding	58%	120%
107874	102	Coding	61%	100%
107875	103	Coding	92%	112%
107876	104	Coding	127%	137%
107877	105	Coding	No data	No data
107878	106	Coding	54%	112%
17893	27	Coding	31%	61%
17899	33	Coding	56%	117%
100802	65	Coding	47%	78%

Oligonucleotides 107871, 107872, 107873, 107874, 107875, 107877, 107878, 17893 and 17899 were chosen for dose response studies.

Results are shown in Table 20. The effect of these oligonucleotides on human p38α was also determined.

TABLE 20

Dose Response of p38β in T-24 cells to human p38β Chimeric (deoxy gapped) Mixed-backbone Phosphorothioate Oligonucleotides

ISIS #	SEQ ID NO:	ASO Gene Target	Dose	% p38β mRNA Expression	% p38α mRNA Inhibition
Control 118966	107	---	---	100%	100%
107871	99	coding	50 nM	41%	105%
"	"	"	100 nM	42%	132%
"	"	"	200 nM	10%	123%
107872	100	coding	50 nM	71%	124%
"	"	"	100 nM	13%	84%
"	"	"	200 nM	22%	102%
107873	101	coding	50 nM	69%	132%
"	"	"	100 nM	41%	119%
"	"	"	200 nM	23%	131%
107874	102	coding	50 nM	75%	109%
"	"	"	100 nM	34%	99%
"	"	"	200 nM	23%	87%
107875	103	coding	50 nM	82%	93%
"	"	"	100 nM	38%	101%
"	"	"	200 nM	40%	91%
107877	105	coding	50 nM	50%	127%
"	"	"	100 nM	34%	125%
"	"	"	200 nM	22%	106%
107878	106	coding	50 nM	70%	110%

"	"	"	100 nM	43%	109%
"	"	"	200 nM	27%	116%
17893	27	coding	50 nM	28%	88%
"	"	"	100 nM	27%	115%
"	"	"	200 nM	16%	108%
17899	33	coding	50 nM	89%	87%
"	"	"	100 nM	36%	104%
"	"	"	200 nM	15%	80%

These data show that the oligonucleotides designed to target human p38β, do so in a target-specific and dose-dependent manner.

Example 10: Real-time Quantitative PCR Analysis of p38α mRNA Levels

Quantitation of p38α mRNA levels was accomplished by real-time quantitative PCR using the ABI PRISM™ 7600, 7700, or 7900 Sequence Detection System (PE-Applied Biosystems, Foster City, CA) according to manufacturer's instructions. This is a closed-tube, non-gel-based, fluorescence detection system which allows high-throughput quantitation of polymerase chain reaction (PCR) products in real-time. As opposed to standard PCR in which amplification products are quantitated after the PCR is completed, products in real-time quantitative PCR are quantitated as they accumulate. This is accomplished by including in the PCR reaction an oligonucleotide probe that anneals specifically between the forward and reverse PCR primers, and contains two fluorescent dyes. A reporter dye (e.g., FAM or JOE, obtained from either PE-Applied Biosystems, Foster City, CA, Operon Technologies Inc., Alameda, CA or Integrated DNA Technologies Inc., Coralville, IA) is attached to the 5' end of the probe and a quencher dye (e.g., TAMRA,

obtained from either PE-Applied Biosystems, Foster City, CA, Operon Technologies Inc., Alameda, CA or Integrated DNA Technologies Inc., Coralville, IA) is attached to the 3' end of the probe. When the probe and dyes are intact, reporter dye emission is quenched by the proximity of the 3' quencher dye. During amplification, annealing of the probe to the target sequence creates a substrate that can be cleaved by the 5'-exonuclease activity of Taq polymerase. During the extension phase of the PCR amplification cycle, cleavage of the probe by Taq polymerase releases the reporter dye from the remainder of the probe (and hence from the quencher moiety) and a sequence-specific fluorescent signal is generated. With each cycle, additional reporter dye molecules are cleaved from their respective probes, and the fluorescence intensity is monitored at regular intervals by laser optics built into the ABI PRISM™ Sequence Detection System. In each assay, a series of parallel reactions containing serial dilutions of mRNA from untreated control samples generates a standard curve that is used to quantitate the percent inhibition after antisense oligonucleotide treatment of test samples.

Prior to quantitative PCR analysis, primer-probe sets specific to the target gene being measured are evaluated for their ability to be "multiplexed" with a GAPDH amplification reaction. In multiplexing, both the target gene and the internal standard gene GAPDH are amplified concurrently in a single sample. In this analysis, mRNA isolated from untreated cells is serially diluted. Each dilution is amplified in the presence of primer-probe sets specific for GAPDH only, target gene only ("single-plexing"), or both (multiplexing). Following PCR amplification, standard curves of GAPDH and target mRNA signal as a function of dilution are generated from both the single-plexed and multiplexed samples. If both the slope and correlation coefficient of the GAPDH and target signals generated from the multiplexed samples fall within 10%

of their corresponding values generated from the single-plexed samples, the primer-probe set specific for that target is deemed multiplexable. Other methods of PCR are also known in the art.

PCR reagents were obtained from Invitrogen Corporation, (Carlsbad, CA). RT-PCR reactions were carried out by adding 20 μL PCR cocktail (2.5x PCR buffer minus $MgCl_2$, 6.6 mM $MgCl_2$, 375 μM each of dATP, dCTP, dCTP and dGTP, 375 nM each of forward primer and reverse primer, 125 nM of probe, 4 Units RNAse inhibitor, 1.25 Units PLATINUM® Taq, 5 Units MuLV reverse transcriptase, and 2.5x ROX dye) to 96-well plates containing 30 μL total RNA solution (20-200 ng). The RT reaction was carried out by incubation for 30 minutes at 48°C. Following a 10 minute incubation at 95°C to activate the PLATINUM® Taq, 40 cycles of a two-step PCR protocol were carried out: 95°C for 15 seconds (denaturation) followed by 60°C for 1.5 minutes (annealing/extension).

Gene target quantities obtained by real time RT-PCR are normalized using either the expression level of GAPDH, a gene whose expression is constant, or by quantifying total RNA using RiboGreen™ (Molecular Probes, Inc. Eugene, OR). GAPDH expression is quantified by real time RT-PCR, by being run simultaneously with the target, multiplexing, or separately. Total RNA is quantified using RiboGreen™ RNA quantification reagent (Molecular Probes, Inc. Eugene, OR). Methods of RNA quantification by RiboGreen™ are taught in Jones, L.J., et al, (Analytical Biochemistry, 1998, 265, 368-374).

In this assay, 170 μL of RiboGreen™ working reagent (RiboGreen™ reagent diluted 1:350 in 10mM Tris-HCl, 1 mM EDTA, pH 7.5) is pipetted into a 96-well plate containing 30 μL purified, cellular RNA. The plate is read in a CytoFluor 4000 (PE Applied Biosystems) with excitation at 485nm and emission at 530nm.

Probes and primers to human p38α were designed to hybridize to a human p38α sequence, using published sequence information (GenBank accession number L35253, incorporated herein as SEQ ID NO:1). For human p38α the PCR primers were: forward primer: GATGAGTGGAAAAGCCTGAC (SEQ ID NO: 108) reverse primer: CTGCAACAAGAGGCACTTGA (SEQ ID NO: 109) and the PCR probe was: FAM-GATGAAGTCATCAGCTTTGTGCCACCACCCCTTGACCAAGAAGAGATGGA-TAMRA (SEQ ID NO: 110) where FAM is the fluorescent dye and TAMRA is the quencher dye. For human GAPDH the PCR primers were: forward primer: GAAGGTGAAGGTCGGAGTC(SEQ ID NO: 111) reverse primer: GAAGATGGTGATGGGATTTC (SEQ ID NO: 112) and the PCR probe was: 5' JOE-CAAGCTTCCCGTTCTCAGCC- TAMRA 3' (SEQ ID NO: 113) where JOE is the fluorescent reporter dye and TAMRA is the quencher dye.

Probes and primers to mouse p38α were designed to hybridize to a mouse p38α sequence, using published sequence information (GenBank accession number U10871.1, incorporated herein as SEQ ID NO: 114). For mouse p38α the PCR primers were:
forward primer: AAGGGAACGAGAAAACTGCTGTT (SEQ ID NO: 115)
reverse primer: TATTTTAACCAGTGGTATTATCTGACATCCT (SEQ ID NO: 116) and the PCR probe was: FAM-TTGTATTTGTGAACTTGGCTGTAATCTGGTATGCC -TAMRA
(SEQ ID NO: 117) where FAM is the fluorescent reporter dye and TAMRA is the quencher dye. For mouse GAPDH the PCR primers were:
forward primer: GGCAAATTCAACGGCACAGT(SEQ ID NO: 118)
reverse primer: GGGTCTCGCTCCTGGAAGAT(SEQ ID NO: 119) and the PCR probe was: 5' JOE-AAGGCCGAGAATGGGAAGCTTGTCATC- TAMRA 3' (SEQ ID NO: 120) where JOE is the fluorescent reporter dye and TAMRA is the quencher dye.

Probes and primers to rat p38α were designed to hybridize to a rat p38α sequence, using published sequence information (GenBank accession number U73142, incorporated herein as SEQ ID NO: 45). For rat p38α the PCR primers were:
forward primer: ATCATTTGGAGCCCAGAAGGA (SEQ ID NO: 121)
reverse primer: TGGAGCTGGACTGCATACTGA (SEQ ID NO: 122) and the PCR probe was: FAM- CTGGCCAGGCCTCACCGC -TAMRA
(SEQ ID NO: 123) where FAM is the fluorescent reporter dye and TAMRA is the quencher dye. For rat GAPDH the PCR primers were:
forward primer: TGTTCTAGAGACAGCCGCATCTT(SEQ ID NO: 124)
reverse primer: CACCGACCTTCACCATCTTGT(SEQ ID NO: 125) and the PCR probe was: 5' JOE-TTGTGCAGTGCCAGCCTCGTCTCA- TAMRA 3' (SEQ ID NO: 126) where JOE is the fluorescent reporter dye and TAMRA is the quencher dye.

Example 11: Additional Human p38α Oligonucleotide Sequences

Additional antisense oligonucleotides were designed to target human p38α using published sequence (Genbank accession number NM_001315.1, provided herein as SEQ ID NO: 127). Oligonucleotides were synthesized as chimeric oligonucleotides ("gapmers") 20 nucleotides in length, composed of a central "gap" region consisting of ten 2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by five-nucleotide "wings." The wings are composed of 2'-methoxyethyl (2'-MOE) nucleotides. Internucleoside linkages are phosphorothioate (P=S). These oligonucleotide sequences are shown in Table 21. "Target site" indicates the first (5'-most) nucleotide number on the particular target sequence to which the compound binds. The compounds can be analyzed for their effect on human p38α mRNA levels by quantitative real-time PCR as described in other examples herein.

Table 21

Additional chimeric phosphorothioate antisense oligonucleotides targeted to human p38α

ISIS #	Region	Target Sequence Accession #	Target Site	SEQUENCE	SEQ ID NO:
186877	coding	NM_001315.1	1271	GAGCAAAGTAGGCATGTGCA	128
186878	3' UTR	NM_001315.1	2703	GTTTCCGAAGTTTGGGATAT	129
186879	3' UTR	NM_001315.1	2735	GCATTAGTTATTGGGAGTGA	130
186880	3' UTR	NM_001315.1	1671	CCCTGGAGCATCCACAACCT	131
186881	coding	NM_001315.1	1021	TGTACCAGGAAACAATGTTC	132
186882	5' UTR	NM_001315.1	326	CGGGCAAGAAGGTGGCCCTG	133
186883	3' UTR	NM_001315.1	3296	ATCGCCATCAGTCTGCCTCC	134
186884	3' UTR	NM_001315.1	2312	TGACATCAAGAACCTGCTTC	135
186885	3' UTR	NM_001315.1	2134	GGCCCACAAGCAGCTGTCCA	136
186886	3' UTR	NM_001315.1	3063	TGAAAACGACACTTCTCCAC	137
186887	3' UTR	NM_001315.1	3307	GGTGAGAGGGAATCGCCATC	138
186888	3' UTR	NM_001315.1	2007	ATACTGTCAAGATCTGAGAA	139
186889	3' UTR	NM_001315.1	2702	TTTCCGAAGTTTGGGATATT	140
186890	3' UTR	NM_001315.1	2205	AGAGAGACGCACATATACGC	141
186891	3' UTR	NM_001315.1	1516	CAAGAGGCACTTGAATAATA	142
186892	coding	NM_001315.1	638	ATTCCTCCAGAGACCTTGCA	143
186893	3' UTR	NM_001315.1	2848	AAGACACCTTGTTACTTTTT	144
186894	3' UTR	NM_001315.1	2989	TGCCCTTTCTCCCCATCAAA	145
186895	coding	NM_001315.1	1096	TGGCATCCTGTTAATGAGAT	146
186896	3' UTR	NM_001315.1	1477	AAGGCCTTCCCCTCACAGTG	147
186897	3' UTR	NM_001315.1	3728	AATAGGCTTTATTTTAACCA	148
186898	3' UTR	NM_001315.1	2455	ACCCAAGAAGTCTTCACTGG	149
186899	3' UTR	NM_001315.1	3135	TTTCTTATTACACAAAAGGC	150
186900	3' UTR	NM_001315.1	3445	GGAAATCACACGAGCATTTA	151
186901	coding	NM_001315.1	794	GGTCCCTGTGAATTATGTCA	152
186902	3' UTR	NM_001315.1	3112	AATATATGAGTCCTCATGTA	153
186903	3' UTR	NM_001315.1	3511	CTAACACGTATGTGGTCACA	154
186904	3' UTR	NM_001315.1	2984	TTTCTCCCCATCAAAAGGAA	155
186905	coding	NM_001315.1	727	CTGAACATGGTCATCTGTAA	156
186906	3' UTR	NM_001315.1	3681	ATAACTGATTACAGCCAAGT	157
186907	3' UTR	NM_001315.1	2959	TTCTCAAAGGGATTCCTACA	158
186908	coding	NM_001315.1	678	TCTGCCCCCATGAGATGGGT	159
186909	coding	NM_001315.1	540	TTCGCATGAATGATGGACTG	160
186910	coding	NM_001315.1	1275	TACTGAGCAAAGTAGGCATG	161
186911	coding	NM_001315.1	1336	GTCCCTGCTTTCAAAGGACT	162
186912	coding	NM_001315.1	577	CATATGTTTAAGTAACCGCA	163
186913	3' UTR	NM_001315.1	2963	CACATTCTCAAAGGGATTCC	164

Additional antisense oligonucleotides were designed to target human p38α using published sequence (Genbank accession

number NM_001315.1, provided herein as SEQ ID NO: 127. Oligonucleotides were synthesized as oligonucleotides comprised of 2'-deoxynucleotides and phosphodiester internucleoside linkages (P=O). These oligonucleotide sequences are shown in Table 22. "Target site" indicates the first (5'-most) nucleotide number on the particular target sequence to which the compound binds.

Table 22

Additional phosphodiester oligonucleotides targeted to p38α

ISIS #	Region	Target Sequence Accession #	Target Site	SEQUENCE	SEQ ID NO
169107	coding	NM_001315.1	1420	GGACTCCATCTCTTCTTGGTCAA	165
336747	3' UTR	NM_001315.1	1454	GAAGTGGGATCAACAGAACAGAAA	166
336750	coding	NM_001315.1	436	AGCCCACTGGAGACAGGTTCT	167

Example 12: Mouse and rat p38α antisense oligonucleotides

Antisense oligonucleotides were designed to target mouse p38α using published sequences (Genbank accession number U10871.1, provided herein as SEQ ID NO: 114, GenBank accession number D83073.1, provided herein as SEQ ID NO: 168, GenBank accession number AA002328.1, provided herein as SEQ ID NO: 169, GenBank accession number AF128892.1, provided herein as SEQ ID NO: 170, GenBank accession number BY159314.1, provided herein as SEQ ID NO: 171 and Genbank accession number BY257628.1, provided herein as SEQ ID NO: 172). These compounds are shown in the tables included in this example.

Antisense oligonucleotides were also designed to target rat p38α using published sequences (GenBank accession number U73142, provided herein as SEQ ID NO: 45, and Genbank accession number U91847.1, provided herein as SEQ ID NO: 173). These compounds are shown in the tables in this example.

Oligonucleotides were synthesized as chimeric oligonucleotides ("gapmers") 20 nucleotides in length, composed of a central "gap" region consisting of ten

2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by five-nucleotide "wings." The wings are composed of 2'-methoxyethyl (2'-MOE) nucleotides. Internucleoside linkages are phosphorothioate (P=S). In Table 23, "Target site" indicates the first (5'-most) nucleotide number on the particular target sequence to which the compound binds.

The compounds in Table 23 were analyzed for their effect on mouse p38α mRNA levels by quantitative real-time PCR as described in other examples herein. Data are averages from two experiments in which bEND.3 cells were treated with the antisense oligonucleotides of the present invention and are presented in the column labeled "% inhib, mouse p38α". If present, "N.D." indicates "no data". ISIS 18078 (GTGCGCGCGAGCCCGAAATC, SEQ ID NO: 174) was used as a scrambled control oligonucleotide.

The compounds in Table 23 were also analyzed for their effect on rat p38α mRNA levels in NR-8383 cells by quantitative real-time PCR as described in other examples herein. The rat normal lung alveolar macrophage cell line NR-8383 was obtained from the American Type Culture Collection (Manassas, VA). NR-8383 cells were routinely cultured in Ham's F12 medium (Gibco/Life Technologies, Gaithersburg, MD) supplemented with 10% fetal bovine serum (Gibco/Life Technologies, Gaithersburg, MD), and 1% Penicillin/Streptomycin (Gibco/Life Technologies, Gaithersburg, MD). Cells were routinely passaged by trypsinization and dilution when they reached 90% confluence. For transfection with oligonucleotides, NR-8383 cells were plated on 24 well plates at a density of $4x10^4$ cells/cm2 ($8.0x10^4$ cells/well) in serum-free F12 Nutrient Medium (Gibco/Life Technologies, Gaithersburg, MD). After 2 hours, media was removed and replaced with 400ul of Ham's F12 Nutrient Medium supplemented with 15% fetal bovine serum and

1% Penicillin/Streptomyocin. Cells were then transfected with 300 nM of antisense oligonucleotides mixed with FuGENE 6 Transfection Reagent (Roche Applied Science, Indianapolis, IN) for 24 hours, after which mRNA was quantitated as described in other examples herein. Data are averages from two experiments in which NR-8383 cells were treated with the antisense oligonucleotides of the present invention and are presented in the column labeled "% inhib, rat p38α". If present, "N.D." indicates "no data". ISIS 18078 (GTGCGCGCGAGCCCGAAATC, SEQ ID NO: 174) was used as a scrambled control oligonucleotide.

One additional compound, ISIS 186911 (SEQ ID NO: 143), targeted to human p38α, was also tested for its effect on mouse and rat p38α mRNA expression in bEND.3 cells and NR-8383 cells, respectively.

An asterisk (*) adjacent to the ISIS oligonucleotide number in Table 23 indicates that the oligonucleotide targets human, mouse and rat p38α sequences. Compounds in Table 23, with the exception of ISIS 101753, ISIS 320119, ISIS 320120 and 320121 target both mouse and rat p38α.

Table 23

Inhibition of mouse and rat p38α by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap

ISIS #	Region	Target Sequence Accession #	Target Site	Sequence	% Inhib, mouse p38 α	% Inhib, rat p38 α	Seq ID NO
100864*	coding	L35253	538	TCCAACAGACCAATCACATT	83	57	82
101753	start codon	U73142	1	CTGCGACATTTTCCAGCGGC	64	43	175
101755*	coding	U10871.1	1226	CATCATCAGGGTCGTGGTAC	84	74	176
101757*	coding	U10871.1	1336	AGGTGCTCAGGACTCCATTT	88	53	177
186911*	coding	NM_001315.1	1336	GTCCCTGCTTTCAAAGGACT	81	40	178
306022*	coding	U73142	781	GGCCAGAGACTGAATGTAGT	78	53	179
320103*	coding	U10871.1	315	AGCTCCTGCCGGTAGAACGT	81	55	180
320104*	coding	U10871.1	405	TCAAAAGCAGCACACACCGA	82	42	181
320105*	coding	U10871.1	417	CCCGTCTTTGTATCAAAAGC	89	59	182
320106*	coding	U10871.1	453	AACGGTCTCGACAGCTTCTT	91	67	183

320107*	coding	U10871.1	483	TAGGTCCTTTTGGCGTGAAT	84	60	184
320108*	coding	U10871.1	600	AGATGGGTCACCAGGTACAC	61	57	185
320109*	coding	U10871.1	609	GCCCCCATGAGATGGGTCAC	69	34	186
320110*	coding	U10871.1	807	TCATCAGTGTGCCGAGCCAG	87	54	187
320111*	coding	U10871.1	930	GTCAACAGCTCAGCCATGAT	86	55	188
320112*	coding	U10871.1	940	CGTTCTTCCGGTCAACAGCT	93	58	189
320113*	coding	U10871.1	967	ATCAATATGGTCTGTACCAG	35	9	190
320114*	coding	U10871.1	987	CTTAAAATGAGCTTCAACTG	71	60	191
320115*	coding	U10871.1	1001	GGGTTCCAACGAGTCTTAAA	67	53	192
320116*	coding	U10871.1	1019	TCAGAAGCTCAGCCCCTGGG	95	73	193
320117*	coding	U10871.1	1030	GGAGATTTTCTTCAGAAGCT	72	55	194
320118*	coding	U10871.1	1040	CAGACTCTGAGGAGATTTTC	47	69	195
320119	coding	U10871.1	1050	TAGTTTCTTGCAGACTCTGA	53	32	196
320120	coding	U10871.1	1060	AGACTGAATGTAGTTTCTTG	74	39	197
320121	coding	U10871.1	1083	TTCATCTTCGGCATCTGGGC	83	57	198
320122	coding	U10871.1	1093	ATTTGCGAAGTTCATCTTCG	73	48	199
320123	coding	U10871.1	1103	CAATAAATACATTTGCGAAG	79	32	200
320124	coding	U10871.1	1113	GGATTGGCACCAATAAATAC	29	31	201
320125	coding	U10871.1	1176	GCTGCTGTGATCCTCTTATC	67	63	202
320126	coding	U10871.1	1196	AGGCATGCGCAAGAGCTTGG	90	69	203
320127	coding	U10871.1	1206	TGAGCAAAGTAGGCATGCGC	73	56	204
320128	coding	U10871.1	1260	TCAAAGGACTGGTCATAAGG	79	37	205
320129	coding	U10871.1	1351	CATTTCTTCTTGGTCAAGGG	69	65	206
320130	stop codon	U10871.1	1358	AGGACTCCATTTCTTCTTGG	81	61	207
320131	3'UTR	U10871.1	1406	CTTCCCCTCACAGTGAAGTG	92	39	208
320132	3'UTR	U10871.1	1432	TATTTGGAGAGTTCCCATGA	85	56	209
320133	3'UTR	U10871.1	1442	ACTTGAATGGTATTTGGAGA	52	61	210
320134	3'UTR	U10871.1	1452	AACAAGAGGCACTTGAATGG	85	74	211
320135	3'UTR	U10871.1	1480	ACCCCCTTCCACCATGAAGG	95	47	212
320136	3'UTR	U10871.1	1608	AGCAGGCAGACTGCCAAGGA	83	34	213
320137	3'UTR	U10871.1	1663	CACACACATCCCTAAGGAGA	80	44	214
320138	3'UTR	U10871.1	1745	TAAAGGCAGGGCCACAGGAG	87	46	215
320139	3'UTR	U10871.1	1771	GCAGCCTCTCTCTGTCACTG	87	61	216
320140	3'UTR	U10871.1	1791	GGGATAGCCTCAGACCTGAA	61	37	217
320141	3'UTR	U10871.1	1801	GCATGGCTGAGGGATAGCCT	83	73	218
320142	3'UTR	U10871.1	1828	GAGCCAGTTGGTTCTCTTGG	85	53	219
320143	3'UTR	U10871.1	1910	AGGCACAAACAGACTGACAG	88	54	220
320144	3'UTR	U10871.1	1917	CCTTTTAAGGCACAAACAGA	83	39	221
320145	3'UTR	U10871.1	2138	GACCTCTGCACTGAGGTGAA	52	44	222
320146	3'UTR	U10871.1	2147	GGCACTGGAGACCTCTGCAC	74	57	223
320147	3'UTR	U10871.1	2228	AGAGCACAGCATGCAAACAC	66	43	224
320148	3'UTR	U10871.1	2259	CCAGGGCTTCCAGAAGACAG	78	33	225
320149	3'UTR	U10871.1	2576	AAGGAGCTCCTGGCTTCAGG	74	25	226
320150	3'UTR	U10871.1	2738	GGATTCCTACAACATACAAA	82	62	227
320151	3'UTR	U10871.1	2758	GAAGGAACCACACTCTCTAA	90	47	228
320152	3'UTR	U10871.1	2778	TTTGCCCTTTCTCCCCATCA	93	66	229
320153	3'UTR	U10871.1	2791	AATATTAAAATAATTTGCCC	0	22	230
320154	3'UTR	U10871.1	2817	TCATGTTTATAAAGGTGAAA	52	50	231
320155	3'UTR	U10871.1	2827	CCCTGAGGATTCATGTTTAT	93	73	232
320156	3'UTR	U10871.1	2930	GGAATTGGCTTTACACTTTC	91	64	233
320157	3'UTR	U10871.1	2941	CGTCCAACACTGGAATTGGC	96	71	234
320158	3'UTR	U10871.1	3042	CCTTCTGGGCTCCAAATGAT	91	71	235
320159	3'UTR	U10871.1	3386	TCTGACATCCTATGGCATAC	94	69	236
320160	coding	D83073.1	900	GTTAATATGGTCTGTACCAG	53	43	237
320161	coding	D83073.1	910	GCTGAAGCTGGTTAATATGG	80	66	238
320162	coding	D83073.1	920	CGCATTATCTGCTGAAGCTG	92	62	239
320163	coding	D83073.1	955	TGTTAATGAGATAAGCAGGG	0	40	240
320164	coding	D83073.1	965	CTTGGCATCCTGTTAATGAG	80	73	241
320165	coding	D83073.1	975	TGCCTCATGGCTTGGCATCC	81	53	242

320166	coding	D83073.1	991	ACTGAATGTAGTTTCTTGCC	53	35	243
320167	5'UTR	AA002328.1	155	CTTGCCTGTAAAAACACAGA	7	11	244
320168	stop codon	AF128892.1	1059	TCACCTCATGGCTTGGCATC	83	56	245
320169	stop codon	AF128892.1	1066	TTTGTTCTCACCTCATGGCT	92	64	246
320170	3'UTR	AF128892.1	1132	TGCTGGCTATACACAGACAC	83	55	247
320171	intron	BY159314.1	58	TGGAAAACTGTTTTGTCAAA	35	2	248
320172	intron	BY257628.1	39	ACTCTCGCGAGAACAGCTCC	39	0	249
320173	intron	BY257628.1	72	TCCCACAGGCAGCGGCCGGG	16	0	250
320174	intron	BY257628.1	97	CCCGCTTGGGCTCCAGTGGC	62	29	251

All compounds in Table 23 inhibited either mouse or rat p38α RNA expression by at least 10%. Compounds with SEQ ID NO: 82, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 231, 232, 233, 234, 235, 236, 237, 238, 239, 241, 242, 243, 245, 246, 247 and 251 inhibited expression of both mouse and rat p38α by at least 10%.

Additional antisense oligonucleotides were designed to target mouse p38α using published sequences (Genbank accession number U10871.1, provided herein as SEQ ID NO: 114). Oligonucleotides are composed of 2'-deoxynucleotides. Internucleoside linkages are phosphorodiester (P=O). These oligonucleotide sequences are shown in Table 24. "Target site" indicates the first (5'-most) nucleotide number on the particular target sequence to which the compound binds.

Table 24

Antisense oligonucleotides targeted to mouse p38α having 2'-deoxynucleotides and phosphodiester linkages

ISIS #	Region	Target Sequence Accession #	Start Site	SEQUENCE	SEQ ID NO
137934	3' UTR	U10871.1	3331	GCAGTTTTCTCGTTCCCTTG	252
264006	coding	U10871.1	1207	CTGAGCAAAGTAGGCATGCG	253
320184	3' UTR	U10871.1	2306	GGAGGCAATGTGGACAGGAA	254
279221	coding	U10871.1	521	CATTTTCGTGTTTCATGTGCTTC	255

326403	3' UTR	U10871.1	3395	TATTTTAACCAGTGGTATTATCTG ACATCCT	256

Additional antisense oligonucleotides were designed to target mouse p38α using published sequences (Genbank accession number U10871.1, provided herein as SEQ ID NO: 114). Oligonucleotides were synthesized as chimeric oligonucleotides ("gapmers") 20 nucleotides in length, composed of a central "gap" region consisting of ten 2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by five-nucleotide "wings." The wings are composed of 2'-methoxyethyl (2'-MOE) nucleotides. Internucleoside linkages in the central gap region are phosphorothioate (P=S), and internucleoside linkages in the wings are phosphodiester (P=O). These oligonucleotide sequences are shown in Table 25. "Target site" indicates the first (5'-most) nucleotide number on the particular target sequence to which the compound binds.

Table 25

Chimeric oligonucleotides targeted to mouse p38α having 2'-MOE wings and a deoxy gap and mixed phophorothioate and phosphodiester internucleoside linkages

ISIS #	Region	Target Sequence Accession #	Start Site	SEQUENCE	SEQ ID NO
101369	start codon	U10871.1	286	CTGCGACATCTTCCAGCGGC	257
101370	coding	U10871.1	646	GGTCAGCTTCTGGCACTTCA	258
101372	3' UTR	U10871.1	1609	AAGCAGGCAGACTGCCAAGG	259

Additional antisense oligonucleotides were designed to target rat p38α using published sequences (GenBank accession number U73142, provided herein as SEQ ID NO: 45, and GenBank accession number U91847.1, provided herein as SEQ ID NO: 173). Oligonucleotides are composed of 2'-deoxynucleotides. Internucleoside linkages are phosphorodiester (P=O). These

oligonucleotide sequences are shown in Table 26. "Target site" indicates the first (5'-most) nucleotide number on the particular target sequence to which the compound binds.

Table 26

Antisense oligonucleotides targeted to rat p38α having 2'-deoxynucleotides and phosphodiester linkages

ISIS #	Region	Target Sequence Accession #	Start Site	SEQUENCE	SEQ ID NO
336744	coding	U91847.1	902	AGGCATGCGCAAGAGCTT	260
336741	coding	U91847.1	66	GGGACAGGTTCTGGTATCGC	261
257014	coding	U91847.1	224	TCTCGTGCTTCATGTGCTTCA	262
320187	3' UTR	U73142	2800	TGGAGCTGGACTGCATACTGA	263

Additional antisense oligonucleotides were designed to target rat p38α using published sequences (GenBank accession number U73142, provided herein as SEQ ID NO: 45). Oligonucleotides were synthesized as chimeric oligonucleotides, composed 2'-deoxynucleotides and 2'-methoxyethyl (2'-MOE) nucleotides (indicated in bold type in Table 27). Internucleoside linkages in the central gap region are phosphorothioate (P=S), and internucleoside linkages in the wings are phosphodiester (P=O). These oligonucleotide sequences are shown in Table 27. "Target site" indicates the first (5'-most) nucleotide number on the particular target sequence to which the compound binds.

Table 27

Chimeric oligonucleotides targeted to rat p38α having 2'-MOE wings and a deoxy gap and mixed phophorothioate and phosphodiester internucleoside linkages

ISIS #	Region	Target Sequence Accession #	Start Site	SEQUENCE	SEQ ID NO

111831	coding	U73142	941	CATCAGGGTCGTGGTAC	264
111830	coding	U73142	942	CATCATCAGGGTCGT	265

Example 13: Mouse model of allergic inflammation

In the mouse model of allergic inflammation, mice were sensitized and challenged with aerosolized chicken ovalbumin (OVA). Airway responsiveness was assessed by inducing airflow obstruction with a methacholine aerosol using a noninvasive method. This methodology utilized unrestrained conscious mice that are placed into the main chamber of a plethysmograph (Buxco Electronics, Inc., Troy, NY). Pressure differences between this chamber and a reference chamber were used to extrapolate minute volume, breathing frequency and enhanced pause (Penh). Penh is a dimensionless parameter that is a function of total pulmonary airflow in mice (i.e., the sum of the airflow in the upper and lower respiratory tracts) during the respiratory cycle of the animal. The lower the Penh, the greater the airflow. This parameter closely correlates with lung resistance as measured by traditional invasive techniques using ventilated animals (Hamelmann et al., 1997). Dose-response data were plotted as raw Penh values to increasing concentrations of methacholine. This system was used to test the efficacy of an antisense oligonucleotide targeted to mouse p38α (ISIS 101757; SEQ ID NO: 177). Six-base -mismatched p38α oligonucleotide (ISIS 101758; SEQ ID NO: 266) was used as a negative control.

There are several important features common to human asthma and the mouse model of allergic inflammation. One of these is pulmonary inflammation, in which cytokine expression and Th2 profile is dominant. Another is goblet cell hyperplasia with increased mucus production. Lastly, airway hyperresponsiveness (AHR) occurs resulting in increased sensitivity to cholinergic receptor agonists such as acetylcholine or methacholine. The compositions and methods

of the present invention may be used to treat AHR and pulmonary inflammation. The combined use of antisense oligonucleotides targeted to human p38 MAP kinase with one or more conventional asthma medications including, but not limited to, montelukast sodium (Singulair™), albuterol, beclomethasone dipropionate, triamcinolone acetonide, ipratropium bromide (Atrovent™), flunisolide, fluticasone propionate (Flovent™) and other steroids is also contemplated.

Ovalbumin-induced allergic inflammation

For intratracheal administration of ISIS 101757, female Balb/c mice (Charles Rivers Laboratory, Taconic Farms, NY) were maintained in micro-isolator cages housed in a specific pathogen-free (SPF) facility. The sentinel cages within the animal colony surveyed negative for viral antibodies and the presence of known mouse pathogens. Mice were sensitized and challenged with aerosolized chicken OVA. Briefly, 20 μg alum-precipitated OVA was injected intraperitoneally on days 0 and 14. On day 24, 25 and 26, the animals were exposed for 20 minutes to 1.0% OVA (in saline) by nebulization. The challenge was conducted using an ultrasonic nebulizer (PulmoSonic, The DeVilbiss Co., Somerset, PA). Animals were analyzed about 24 hours following the last nebulization using the Buxco electronics Biosystem. Lung function (Penh), lung histology (cell infiltration and mucus production), target mRNA reduction in the lung, inflammation (BAL cell type & number, cytokine levels), spleen weight and serum AST/ALT were determined.

For the aerosol studies, the protocol described above was slightly modified. Male Balb/c mice were injected IP with OVA (20 μg) in aluminum hydroxide on days 0 and 14. Aerosol dosing was performed with nebulized sterile saline, antisense oligonucleotide or mismatched control oligonucleotide using

25, 125 and 250 µg/ml solutions (5 mg/kg) for 30 min. on days 14-20 in a closed chamber. Aerosol lung challenge was carried out with nebulized saline or 1% OVA for 20 min. on days 18, 19 and 20. BAL fluid was collected at 24 hr post-last lung challenge (cell differentials) or at 2-12 h post-challenge (cytokine analysis). AHR was measured 24 hours after OVA challenge. Mice were exposed to aerosolized methacholine 24 hr post-last lung challenge from 2-80 mg/ml for 3 min. until a 200% increase in Penh was achieved.

Intratracheal Oligonucleotide administration

Antisense oligonucleotides (ASOs) were dissolved in saline and used to intratracheally dose mice every day, four times per day, from days 15-26 of the OVA sensitization and challenge protocol, or used as an aerosol. Specifically, the mice were anesthetized with isofluorane and placed on a board with the front teeth hung from a line. The nose was covered and the animal's tongue was extended with forceps and 25 µl of various doses of ASO, or an equivalent volume of saline (control) was placed at the back of the tongue until inhaled into the lung.

Mouse antisense oligonucleotides to p38α are phosphorothioates with 2'-MOE modifications on nucleotides 1-5 and 16-20, and 2'-deoxy at positions 6-15. These ASOs were identified by mouse-targeted ASO screening of 10 p38α antisense oligonucleotides by target p38α mRNA reduction in mouse bEND.3 cells, as described in Example 12. Dose-response confirmation led to selection of ISIS 21873 (>70% reduction at 50 nM). ISIS 101757 contains all phosphorothioate linkages, whereas ISIS 21873 is a mixed phosphodiester/phosphorothioate compound. ISIS 101757 had an IC50<50 nM for reducing p38α mRNA in endothelial cells, and an IC50 of about 250 nM in fibroblasts.

Results of aerosol administration

The p38α knock-down effect of ISIS 101757 was confirmed in a mouse T cell line (EL4) and a mouse macrophage cell line (RAW264.7) using Western blotting. ISIS 101757, but not the mismatched control, dose-dependently suppressed methacholine-induced AHR in sensitized mice measured by whole body plethysmography (Fig.1A-1B). The PC200 values for methacholine (Fig. 2) significantly ($P<0.05$) reduced OVA-induced increases in total cell counts and eosinophils recovered in BAL fluid (Fig. 3). In addition, histological studies revealed that ISIS 101757 markedly inhibited OVA-induced inflammatory cell infiltration into the lungs (H&E stain) and mucus hypersecretion in the airway epithelium (PAS stain). ISIS 101757 also significantly ($P<0.05$);lowered blood levels of total IgE, OVA-specific IgE and OVA-specific IgG_1 in sensitized mice as compared to the mismatched control. Oligonucleotide levels of up to 1 μg/g of lung tissue were sufficient to achieve the pharmacological effects described above. The aerosolized ISIS 101757 concentration in mouse lung vs. dose is shown in Fig. 4. There was no significant effect of aerosol oligonucleotide administration of spleen weight. These data indicate that p38α antisense oligonucleotides are useful for the treatment of asthma.

Intratracheal administration results

After intratracheal administration of ISIS 101757 as described above, dose-dependent inhibition of the Penh response to methacholine (50 mg/ml) challenge was observed (Fig. 5). The oligonucleotide concentration (μg/g) in lungs vs. dose is shown in Fig. 6.

RT-PCR analysis

RNA was harvested from experimental lungs removed on day

28 of the OVA protocol. P38α levels were measured by quantitative RT-PCR as described in other examples herein.

Collection of bronchial alveolar lavage (BAL) fluid and blood serum for the determination of cytokine and chemokine levels

Animals were injected with a lethal dose of ketamine, the trachea was exposed and a cannula was inserted and secured by sutures. The lungs were lavaged twice with 0.5 ml aliquots of ice cold PBS with 0.2% FCS. The recovered BAL fluid was centrifuged at 1,000 rpm for 10 min at 4°C, frozen on dry ice and stored at -80°C until used. Luminex was used to measure cytokine levels in BAL fluid and serum.

BAL cell counts and differentials

Cytospins of cells recovered from BAL fluid were prepared using a Shandon Cytospin 3 (Shandon Scientific LTD, Cheshire, England). Cell differentials were performed from slides stained with Leukostat (Fisher Scientific, Pittsburgh, PA). Total cell counts were quantified by hemocytometer and, together with the percent type by differential, were used to calculate specific cell number.

Tissue histology

Before resection, lungs were inflated with 0.5 ml of 10% phosphate-buffered formalin and fixed overnight at 4°C. The lung samples were washed free of formalin with 1X PBS and subsequently dehydrated through an ethanol series prior to equilibration in xylene and embedded in paraffin. Sections (6μ) were mounted on slides and stained with hematoxylin/eosin, massons trichome and periodic acid-schiff (PAS) reagent. Parasagittal sections were analyzed by bright-field microscopy. Mucus cell content was assessed as the airway epithelium staining with PAS. Relative comparisons of mucus content were made between cohorts of animals by counting

the number of PAS-positive airways.

Example 14: Design and screening of duplexed antisense compounds targeting p38α MAP kinase

In accordance with the present invention, a series of nucleic acid duplexes comprising the antisense compounds of the present invention and their complements can be designed to target p38α MAP kinase. The nucleobase sequence of the antisense strand of the duplex comprises at least a portion of an oligonucleotide to p38α MAP kinase as described herein. The ends of the strands may be modified by the addition of one or more natural or modified nucleobases to form an overhang. The sense strand of the dsRNA is then designed and synthesized as the complement of the antisense strand and may also contain modifications or additions to either terminus. For example, in one embodiment, both strands of the dsRNA duplex would be complementary over the central nucleobases, each having overhangs at one or both termini. For example, a duplex comprising an antisense strand having the sequence CGAGAGGCGGACGGGACCG and having a two-nucleobase overhang of deoxythymidine(dT) would have the following structure:

```
  cgagaggcggacgggaccgTT  Antisense Strand (SEQ ID NO: 267)
  ||||||||||||||||||||
TTgctctccgcctgccctggc          Complement (SEQ ID NO: 268)
```

In another embodiment, a duplex comprising an antisense strand having the same sequence CGAGAGGCGGACGGGACCG may be prepared with blunt ends (no single stranded overhang) as shown:

```
cgagaggcggacgggaccg Antisense Strand (SEQ ID NO: 269)
|||||||||||||||||||
gctctccgcctgccctggc Complement (SEQ ID NO: 270)
```

The duplex may be unimolecular or bimolecular, i.e., the sense

and antisense strands may be part of the same molecule (which forms a hairpin or other self structure) or two (or even more) separate molecules.

RNA strands of the duplex can be synthesized by methods disclosed herein or purchased from Dharmacon Research Inc., (Lafayette, CO). Once synthesized, the complementary strands are annealed. The single strands are aliquoted and diluted to a concentration of 50 uM. Once diluted, 30 μL of each strand is combined with 15μL of a 5X solution of annealing buffer. The final concentration of said buffer is 100 mM potassium acetate, 30 mM HEPES-KOH pH 7.4, and 2mM magnesium acetate. The final volume is 75 μL. This solution is incubated for 1 minute at 90°C and then centrifuged for 15 seconds. The tube is allowed to sit for 1 hour at 37°C at which time the dsRNA duplexes are used in experimentation. The final concentration of the dsRNA duplex is 20 uM. This solution can be stored frozen (-20°C) and freeze-thawed up to 5 times.

Once prepared, the duplexed antisense compounds are evaluated for their ability to modulate p38α MAP kinase expression according to the protocols described herein.

Example 15: Design of phenotypic assays and *in vivo* studies for the use of p38α MAP kinase inhibitors

Once p38α MAP kinase inhibitors have been identified by the methods disclosed herein, the compounds are further investigated in one or more phenotypic assays, each having measurable endpoints predictive of efficacy in the treatment of a particular disease state or condition. Phenotypic assays, kits and reagents for their use are well known to those skilled in the art and are herein used to investigate the role and/or association of p38α MAP kinase in health and disease. Representative phenotypic assays, which can be

purchased from any one of several commercial vendors, include those for determining cell viability, cytotoxicity, proliferation or cell survival (Molecular Probes, Eugene, OR; PerkinElmer, Boston, MA), protein-based assays including enzymatic assays (Panvera, LLC, Madison, WI; BD Biosciences, Franklin Lakes, NJ; Oncogene Research Products, San Diego, CA), cell regulation, signal transduction, inflammation, oxidative processes and apoptosis (Assay Designs Inc., Ann Arbor, MI), triglyceride accumulation (Sigma-Aldrich, St. Louis, MO), angiogenesis assays, tube formation assays, cytokine and hormone assays and metabolic assays (Chemicon International Inc., Temecula, CA; Amersham Biosciences, Piscataway, NJ).

In one non-limiting example, cells determined to be appropriate for a particular phenotypic assay (i.e., MCF-7 cells selected for breast cancer studies; adipocytes for obesity studies) are treated with p38α MAP kinase inhibitors identified from the *in vitro* studies as well as control compounds at optimal concentrations which are determined by the methods described above. At the end of the treatment period, treated and untreated cells are analyzed by one or more methods specific for the assay to determine phenotypic outcomes and endpoints.

Phenotypic endpoints include changes in cell morphology over time or treatment dose as well as changes in levels of cellular components such as proteins, lipids, nucleic acids, hormones, saccharides or metals. Measurements of cellular status which include pH, stage of the cell cycle, intake or excretion of biological indicators by the cell, are also endpoints of interest.

Analysis of the genotype of the cell (measurement of the expression of one or more of the genes of the cell) after treatment is also used as an indicator of the efficacy or potency of the p38α MAP kinase inhibitors. Hallmark genes, or

those genes suspected to be associated with a specific disease state, condition, or phenotype, are measured in both treated and untreated cells.

Example 16: Mouse model of allergic inflammation; second aerosol chamber experiment

A second aerosol chamber experiment was conducted with additional animals using methods described in Example 13. Aerosolized p38α antisense oligonucleotide (ISIS 101757, SEQ ID NO: 177), a 6-mismatch negative control (ISIS 101758; SEQ ID NO: 266) or saline (vehicle control) were given to mice daily for 30 minutes in an aerosol chamber from days 14- 20. Aerosol was delivered via a DeVilbiss ultrasonic nebulizer (Model 099HD, Sunrise Medical, Carlsbad CA) with a usable nebulizer output at 6 ml/min and particle sizes < 4 microns. Estimated inhalable doses were 0.3, 1.5 and 3.0 mg/kg from nebulization of 12.5, 62.5 and 125 μg/ml solutions of antisense oligonucleotide, respectively. Using capillary gel electrophoresis (Leeds et al., **1996**, *Anal. Biochem. 235*, 36-43; Geary et al., **1997**, *Drug Metab. Dispos., 25*, 1272-1281), p38α antisense oligonucleotide levels present in lung tissue 24 hours later were determined to be 0.3, 0.8 and 1.1 μg per gram of lung tissue, respectively, indicating dose-dependent accumulation of aerosolized oligonucleotide in lung tissue.

As in the previous aerosol chamber experiment, the p38α antisense oligonucleotide inhibited OVA-induced eosinophil recruitment to the lung, as measured by cell counts in BAL fluid. This effect was mainly due to a significant reduction in eosinophil count in the antisense-treated mice, which was dose-dependent. The numbers of neutrophils, macrophages and lymphocytes was not affected by the p38α antisense compound.

Lung tissue was collected 24 hours after the last OVA challenge. OVA aerosol challenge induced marked infiltration

of inflammatory cells into the peribronchiolar and perivascular connective tissues as compared to saline challenge, with eosinophils constituting the majority of infiltrating inflammatory cells. Inhalation of p38α antisense oligonucleotide (1.5 mg/kg) significantly attenuated the eosinophil-rich leukocyte infiltration as compared to a 6-base mismatch control oligonucleotide. In addition, the OVA-induced mucus secretion within the bronchi of the lung that was a marked observation (along with goblet cell hyperplasia) in the OVA-challenged mice was substantially reduced by the p38α antisense compound (1.5 mg/kg oligonucleotide), but not by the 6-base mismatch control.

To determine the levels of cytokines in vivo, BAL fluid samples were collected 2 hours after the last OVA challenge. IL-4, IL-5, IL-13 and IFNγ levels were measured by ELISA. Mouse IL-4 and IL-5 ELISA were obtained from BD PharMingen (San Diego CA). Mouse IL-13 and IFNγ ELISA were purchased from R&D Systems (Minneapolis MN). Lower limits of detection for IL-4 and IL-4 was 4 pg/ml and for IL-13 and IFNγ were 15.6 pg/ml. OVA inhalation in sensitized mice induced substantial cytokine release into BAL fluid as compared to untreated mice. Treatment of mice with aerosolized p38α antisense (ISIS 101757) significantly reduced levels of Th2 cytokines IL-4, IL-5 and IL-13 in BAL fluid as compared to the 6-mismatch control. In contrast, p38α antisense treatment did not show a significant effect on levels of IFNγ, a Th1 cytokine, in BAL fluid.

The effect of aerosolized p38α antisense compound on the development of AHR (airway hyperresponsiveness) in mice was examined. Sensitized animals challenged with 1% OVA aerosol for 20 minutes daily developed AHR to inhaled methacholine. Airway responsiveness was determined by Penh and was substantially increased in the OVA-challenged group in

response to methacholine provocation, as compared to the saline-challenged group. Inhalation of p38α antisense oligonucleotide (ISIS 101757) significantly reduced AHR to inhaled methacholine in a dose-dependent manner as in a previous experiment. This suggests that the decreased immune-mediated pathology observed in mice treated with p38α antisense compound resulted in decreased airway smooth muscle constriction as well.

To verify that the effects of the inhaled p38α antisense compound on lung inflammatory and airway responses in the mouse asthma model were mediated by p38α knockdown, the effects of the antisense compound on p38α gene expression in BAL fluid cells and peri-bronchial lymph node cells were examined. The level of p38α mRNA was significantly reduced in both BAL fluid cells (over 50% reduction in p38α mRNA) and peri-bronchial lymph node cells (over 60% reduction in p38α mRNA) of p38α antisense-treated mice (3.0 mg/kg) as compared to mice treated with mismatch control.

Example 17: Nose-only aerosol exposure of mice to p38α antisense oligonucleotide is effective

To determine whether nose-only exposure of mice would result in similar pharmacology to that observed with the aerosol chamber, key endpoints were reproduced using a nose-only delivery system known in the art. Silbaugh et al., **1987**, *J. Pharm. Methods, 18,* 295-303. Male Balb/c mice (25 grams, Charles River Laboratories) were sensitized with an i.p. injection (100 µl) of 20 µg OVA emulsified in 2 mg of Imject Alum (Pierce) on days 0 and 14. The mice were subsequently challenged with aerosolized OVA (1%) for 20 minutes on days 24 to 26. Different concentrations of antisense oligonucleotides (estimated inhalable doses of 3.3, 33, and 333 µg/kg) were

administered by aerosol delivery for 5 days (days 17, 19, 21, 24 and 26). Aerosol administration of the oligonucleotides was achieved by means of a nose-only inhalation system. Silbaugh et al., **1987**, *J. Pharm. Methods*, *18*, 295-303. Particle size range was 0.9-1.2 μm. Oligonucleotide deposition in the lungs was measured using a quantitative hybridization-dependent nuclease ELISA method (Yu et al., **2002**, *Anal. Biochem.*, *304*, 19-25. Exposure of mice to aerosolized p38α antisense oligonucleotide resulted in 11.5, 80.3 and 324 ng/g antisense oligonucleotide (ISIS 101757; SEQ ID NO: 177) per gram of lung tissue at estimated inhalable doses of 3.3, 33 and 333 μg/kg. p38α antisense oligonucleotide delivered at these doses via this apparatus produced pronounced inhibition of BAL eosinophilia and AHR in a dose-related manner and also suppressed mucus overproduction (determined by PAS staining). Lung histopathology also showed reduction of tissue eosinophilia and mucus.

Example 18: Further characterization of p38α antisense effects

The active antisense oligonucleotide against mouse p38α was further characterized for potency and specificity for the α isoform. Following lipofectin-mediated transfection of b.END cells, the p38α antisense compound reduced basal mRNA level of p38α in a dose-dependent manner, as determined by RT-PCR as in above examples. p38α mRNA was inhibited by approximately 30% at 1 nM oligonucleotide concentration, by approximately 62% at 5 nM oligonucleotide, by approximately 75% at 10 nM oligonucleotide and by approximately 83% at 25 nM oligonucleotide concentration. The IC50 was thus determined to be in the low nM range. p38α protein levels were also shown to be inhibited in a dose-dependent manner. To confirm an antisense mechanism of p38α reduction, the ISIS 101757 sequence was tested at the same concentration range in

parallel with oligonucleotides containing 1, 2, 4, or 6 mismatches to the ISIS 101757 target site. Activity was compromised in accordance with increasing number of mismatched bases in the sequence, indicating the importance of RNA hybridization for the inhibitory effect. The 1-mismatch sequence had an IC50 in the 5-10 nM range, the 2-mismatch sequence had an IC50 near 25 nM and the 4- and 6-mismatch sequences did not inhibit by 50% at any of these concentrations. An antisense oligonucleotide with the same sequence as ISIS 101757 but with 2'-O-methoxyethyl modifications at every position was also without effect, suggesting that the ISIS 101757-mediated target reduction is dependent upon RNase H1. Evaluation of p38β mRNA levels in b.END cells treated with ISIS 101757 showed no change in expression, suggesting specificity of the p38α antisense oligonucleotide for the α-isoform.

Example 19: Additional antisense compounds targeted to human p38α

An additional set of antisense oligonucleotides were designed to target human p38α. Human p38α target sequences are: Genbank accession number L35253, provided herein as SEQ ID NO: 1; Genbank accession number NM_001315.1, provided herein as SEQ ID NO: 127; accession number NM_139012.1. which uses exons 1 - 8, exon 8a (a unique exon) and exons 10 - 12 (skips exon 9), provided herein as SEQ ID NO: 271; accession number NM_139013.1, which uses exons 1 - 8, exon 8a and exon 10a (extends exon 10 in the 3' direction), provided herein as SEQ ID NO: 272; accession number NM_139014.1, which uses exons 1 - 8, exon 8a and exons 11 - 12 (skips exons 9 and 10) , provided herein as SEQ ID NO: 273; nucleotides 26792300-26876062 of the genomic sequence with accession number NT_007592.13, provided herein as SEQ ID NO: 274; and BG898314.1, which extends 5' from SEQ ID NO: 1, provided

herein as SEQ ID NO: 275. Oligonucleotides were synthesized as chimeric oligonucleotides ("gapmers") 20 nucleotides in length, composed of a central "gap" region consisting of eight 2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by six-nucleotide "wings." The wings are composed of 2'-methoxyethyl (2'-MOE) nucleotides. The internucleoside (backbone) linkages are phosphorothioate (P=S) throughout the oligonucleotide. All 2'-MOE cytosines were 5-methyl-cytosines. These oligonucleotide sequences are shown in Table 28. These were tested in T-24 cells for ability to reduce human p38α mRNA levels, as measured by RT-PCR as in other examples herein. "Target site" indicates the first (5'-most) nucleotide number on the particular target nucleic acid to which the oligonucleotide binds. Also shown in Table 28 is the species to which each of the oligonucleotides is targeted. Oligo concentration was 75 nM.

Table 28

Activity of human p38α antisense compounds in T-24 cells

Isis No	Sequence	Target site	Target sequence SEQ ID NO:	% inhib	Species	SEQ ID NO
100872	ttctcttatctgagtccaat	1164	1	61	Human, Chimp	90
186888	atactgtcaagatctgagaa	2007	127	91	Human	139
186891	caagaggcacttgaataata	1516	127	68	Human	142
186902	aatatatgagtcctcatgta	3112	127	85	Human	153
320131	cttcccctcacagtgaagtg	1472	127	92	Human, Mouse, Rat	208
320152	tttgccctttctccccatca	2991	127	69	Human, Mouse, Rat, Rattus sp.	229
320153	aatattaaaataatttgccc	3004	127	51	Human, Mouse, Rat, Rattus sp.	230
342597	ctgctgggcttcagctcgga	74	1	0	Human	276

342598	taaggctccagtggtcgcgg	5	127	51	Human	277
342599	ggctgcgtcgcagtactccc	45	127	82	Human	278
342600	gccgcagcggctggatgtgc	171	127	60	Human	279
342601	agccgccgggcaagaaggtg	332	127	52	Human	280
342602	ccacaacctcctgtaaagtc	1660	127	81	Human	281
342603	gcctgagccaactctcagaa	1712	127	93	Human	282
342604	aggacagcagctcttgtctg	1731	127	77	Human	283
342605	caaaagcatgaccgggattg	1796	127	97	Human	284
342606	aggagaagccaaagtggcaa	1813	127	76	Human, Mouse	285
342607	tgaagcaaccagaaggtatg	1898	127	71	Human	286
342608	caggtctgaagcaaccagaa	1904	127	93	Human	287
342609	ggctgtacgtatcactgagg	1932	127	87	Human	288
342610	agaagccagttggtcctttt	1953	127	94	Human	289
342611	atactaagcaagttaatcac	1985	127	28	Human	290
342612	tctccttttaaggcacaaac	2045	127	96	Human, Rat	291
342613	ctgcagtcttttaactatct	2076	127	94	Human	292
342614	tctcgacttgcccggctcag	2107	127	95	Human	293
342615	agccctctcgacttgcccgg	2112	127	93	Human	294
342616	ctatgaaggctgcctgatta	2159	127	80	Human	295
342617	aggtgaagggtaagcagaga	2253	127	59	Human	296
342618	ttcaagaaacctctgcacca	2274	127	48	Human	297
342619	aacctgcttctgactactgg	2302	127	87	Human	298
342620	tacatgacatcaagaacctg	2316	127	41	Human	299
342621	ggacaagcagctgtgcatgc	2398	127	82	Human	300
342622	agagcaggacaagcagctgt	2404	127	90	Human	301
342623	gcctcctgaagagagcagga	2415	127	88	Human	302
342624	aagtcttcactggcaaacct	2448	127	90	Human	303
342625	atgggatctaaactacccaa	2469	127	83	Human	304
342626	gccataatatcagctgaggt	2492	127	93	Human	305
342627	gggctgaagagaggtgatat	2517	127	87	Human	306
342628	ttcaacacagaatagcacta	2538	127	75	Human	307
342629	catcaaaagcacctgaagta	2567	127	72	Human	308
342630	taaaaatgctatacatccac	2611	127	29	Human	309
342631	ttggttgaaaacagatggca	2635	127	85	Human	310
342632	tcagcatttcttagcattag	2748	127	94	Human	311
342633	gcaaaaggagtttctggcct	2796	127	94	Human	312
342634	ttaaagtaatcatatttaga	2824	127	10	Human	313
342635	ggaaaagacaccttgttact	2852	127	89	Human	314
342636	ttccataggagtggaaaaga	2864	127	0	Human	315
342637	aagggattcctacaatatac	2953	127	62	Human	316
342638	aataatttgccctttctccc	2996	127	57	Human, Mouse, Rat, Rattus sp.	317
342639	tctttataaagttgaaaata	3027	127	48	Human	318
342640	tctccacccctgaggatatt	3050	127	70	Human	319
342641	agttatgaaaacgacacttc	3068	127	81	Human	320
342642	tctgtcacacagccaacact	3171	127	70	Human	321

342643	attgagaaatggaaacacct	3208	127	78	Human	322
342644	cctctggagtacatgtatca	3236	127	85	Human	323
342645	cttgctccagttgactcagg	3270	127	92	Human	324
342646	tttctgtaggaaatcacacg	3453	127	81	Human	325
342647	tacaaaatattcagagcagt	3474	127	92	Human	326
342648	gtatgtggtcacatgtgcaa	3504	127	74	Human	327
342649	cattatgctcagaaaccgaa	3585	127	41	Human	328
342650	tacggcataactgattacag	3687	127	90	Human	329
342651	ctttattttaaccagtggta	3722	127	94	Human, Mouse	330
342652	ataggctttattttaaccag	3727	127	95	Human	331
342653	tgatcaatatggtctgtacc	1035	271	66	Human, Mouse, Rat, Dog	332
342654	aacgagtcttaaaatgagct	1060	271	81	Human, Mouse, Rat, Dog	333
342655	agtttcttgcagactctgag	1115	271	63	Human, Mouse, Rat, Dog	334
342656	tatccatgaggtgaggatat	1217	272	66	Human	335
342657	aagtcgacagagactctgag	1115	273	24	Human	336
342658	cgacactcaccacacagagc	869	274	61	Human	337
342659	gcaacaaggctgtgttgctt	8307	274	86	Human	338
342660	aactacagaggacttccaaa	12666	274	21	Human	339
342661	aataacttacattttcatgt	25424	274	0	Human	340
342662	gagaccaactcatgtaggac	37475	274	70	Human	341
342663	ttcattttaccttcagctca	46692	274	0	Human	342
342664	tgatcaatatctaatggtgg	68582	274	51	Human, Rat	343
342665	atgaaacaaattcagagtgg	69792	274	85	Human	344
342666	tggttaatatcttagatgcc	72783	274	80	Human	345
342667	aacagctcccgggactctcc	99	275	41	Human	346

Antisense compounds with SEQ ID NOs 90, 139, 142, 153, 208, 229, 230, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 341, 343, 344, 345 and 346 inhibited p38α RNA expression by at least 10% in this assay.

Compounds of SEQ ID NOs 90, 139, 142, 153, 208, 229, 230, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288,

289, 291, 292, 293, 294, 295, 296, 298, 300, 301, 302, 303, 304, 305, 306, 307, 308, 310, 311, 312, 314, 316, 319, 320, 321, 322, 323, 324, 325, 326, 327, 329, 330, 331, 332, 333, 334, 335, 337, 338, 341, 343, 344 and 345 gave greater than 50% inhibition of human p38α mRNA expression in this assay.

The compounds shown in the previous table were also screened in A549 cells. The human lung carcinoma cell line A549 is obtained from the American Type Culture Collection (ATCC) (Manassas, VA). A549 cells are routinely cultured in DMEM basal media (Gibco/Life Technologies, Gaithersburg, MD) supplemented with 10% fetal calf serum (Gibco/Life Technologies, Gaithersburg, MD), penicillin 100 units per mL, and streptomycin 100 µg/mL (Gibco/Life Technologies, Gaithersburg, MD). Cells were treated with antisense compounds at a concentration of 50 nM. Results are shown in Table 29.

Table 29

Activity of human p38α antisense compounds in A549 cells

Isis No	Sequence	% inhib	SEQ ID NO
100872	ttctcttatctgagtccaat	42	90
186888	atactgtcaagatctgagaa	74	139
186891	caagaggcacttgaataata	59	142
186902	aatatatgagtcctcatgta	57	153
320131	cttcccctcacagtgaagtg	68	208
320152	tttgccctttctccccatca	47	229
320153	aatattaaaataatttgccc	13	230

342597	ctgctgggcttcagctcgga	0	276
342598	taaggctccagtggtcgcgg	13	277
342599	ggctgcgtcgcagtactccc	62	278
342600	gccgcagcggctggatgtgc	40	279
342601	agccgccgggcaagaaggtg	32	280
342602	ccacaacctcctgtaaagtc	72	281
342603	gcctgagccaactctcagaa	65	282
342604	aggacagcagctcttgtctg	40	283
342605	caaaagcatgaccgggattg	78	284
342606	aggagaagccaaagtggcaa	65	285
342607	tgaagcaaccagaaggtatg	49	286
342608	caggtctgaagcaaccagaa	73	287
342609	ggctgtacgtatcactgagg	67	288
342610	agaagccagttggtcctttt	74	289
342611	atactaagcaagttaatcac	39	290
342612	tctccttttaaggcacaaac	75	291
342613	ctgcagtcttttaactatct	54	292
342614	tctcgacttgcccggctcag	66	293
342615	agccctctcgacttgcccgg	62	294
342616	ctatgaaggctgcctgatta	22	295
342617	aggtgaagggtaagcagaga	51	296
342618	ttcaagaaacctctgcacca	44	297
342619	aacctgcttctgactactgg	61	298
342620	tacatgacatcaagaacctg	38	299
342621	ggacaagcagctgtgcatgc	46	300
342622	agagcaggacaagcagctgt	60	301
342623	gcctcctgaagagagcagga	69	302
342624	aagtcttcactggcaaacct	60	303
342625	atgggatctaaactacccaa	63	304
342626	gccataatatcagctgaggt	60	305
342627	gggctgaagagaggtgatat	33	306
342628	ttcaacacagaatagcacta	51	307
342629	catcaaaagcacctgaagta	61	308
342630	taaaaatgctatacatccac	14	309
342631	ttggttgaaaacagatggca	67	310
342632	tcagcatttcttagcattag	84	311
342633	gcaaaaggagtttctggcct	60	312
342634	ttaaagtaatcatatttaga	21	313
342635	ggaaaagacaccttgttact	50	314
342636	ttccataggagtggaaaaga	7	315
342637	aagggattcctacaatatac	20	316
342638	aataatttgccctttctccc	37	317
342639	tctttataaagttgaaaata	4	318
342640	tctccacccctgaggatatt	56	319
342641	agttatgaaaacgacacttc	60	320
342642	tctgtcacacagccaacact	55	321
342643	attgagaaatggaaacacct	48	322
342644	cctctggagtacatgtatca	48	323
342645	cttgctccagttgactcagg	70	324

342646	tttctgtaggaaatcacacg	69	325
342647	tacaaaatattcagagcagt	70	326
342648	gtatgtggtcacatgtgcaa	20	327
342649	cattatgctcagaaaccgaa	30	328
342650	tacggcataactgattacag	69	329
342651	ctttattttaaccagtggta	77	330
342652	ataggctttattttaaccag	75	331
342653	tgatcaatatggtctgtacc	20	332
342654	aacgagtcttaaaatgagct	44	333
342655	agtttcttgcagactctgag	34	334
342656	tatccatgaggtgaggatat	25	335
342657	aagtcgacagagactctgag	2	336
342658	cgacactcaccacacagagc	20	337
342659	gcaacaaggctgtgttgctt	30	338
342660	aactacagaggacttccaaa	31	339
342661	aataacttacattttcatgt	0	340
342662	gagaccaactcatgtaggac	50	341
342663	ttcattttaccttcagctca	9	342
342664	tgatcaatatctaatggtgg	42	343
342665	atgaaacaaattcagagtgg	72	344
342666	tggttaatatcttagatgcc	52	345
342667	aacagctcccgggactctcc	1	346

Antisense compounds with SEQ ID NOs: 90, 139, 142, 153, 208, 229, 230, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 316, 317, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 337, 338, 339, 341, 343, 344, 345 inhibited p38α RNA expression by at least 10% in this assay.

Compounds with SEQ ID NOs 139, 142, 153, 208, 278, 281, 282, 284, 285, 287, 288, 289, 291, 292, 293, 294, 296, 298, 301, 302, 303, 304, 305, 307, 308, 310, 311, 312, 314, 319, 320, 321, 324, 325, 326, 329, 330, 331, 341, 344 and 345 demonstrated at least 50% inhibition of p38α expression and are preferred.

Example 20: Additional compounds targeted to human p38α

An additional set of antisense oligonucleotides were

designed to target human p38α (Genbank accession no. NM_001315.1; SEQ ID NO: 127). Human p38α target sequences are indicated in the table. Oligonucleotides were synthesized as chimeric oligonucleotides ("gapmers") 20 nucleotides in length, composed of a central "gap" region consisting of eight 2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by six-nucleotide "wings." The wings are composed of 2'-methoxyethyl (2'-MOE) nucleotides. The internucleoside (backbone) linkages are phosphorothioate (P=S) throughout the oligonucleotide. All 2'-MOE cytosines were 5-methyl-cytosines. These oligonucleotide sequences are shown in Table 30. These were tested in A549 cells for ability to reduce human p38α mRNA levels, as measured by RT-PCR as in other examples herein. "Target site" indicates the first (5'-most) nucleotide number on the particular target nucleic acid to which the oligonucleotide binds. Also shown in Table 30 is the species to which each of the oligonucleotides is targeted. Oligo concentration was 50 nM.

Table 30
Activity of antisense oligonucleotides targeted to p38α

Isis No	Sequence	% inhib	Species	Target Site	SEQ ID NO:
342531	GACATTTTCCAGCGGCAGCC	54	Human, Chimp	348	347
342532	TAGAACGTGGGCCTCTCCTG	65	Human, Mouse, Rat, Chimp	369	348
342533	GCCGGTAGAACGTGGGCCTC	40	Human, Mouse, Rat, Chimp	374	349
342534	CGCTCGGGCACCTCCCAGAT	65	Human, Chimp, Dog	411	350
342535	CACTGGAGACAGGTTCTGGT	63	Human, Chimp	433	351
342536	CGCCAGAGCCCACTGGAGAC	46	Human, Chimp	443	352
342537	AGCAGCACACACAGAGCCAT	64	Human, Chimp	466	353
342538	TTTGTGTCAAAAGCAGCACA	62	Human, Chimp, Dog	477	354

342539	TAACCCCGTTTTTGTGTCAA	55	Human, Chimp	487	355
342540	CTGCCACACGTAACCCCGTT	76	Human, Chimp	497	356
342541	TGGACTGAAATGGTCTGGAG	75	Human, Chimp, Dog	527	357
342542	GCATGAATGATGGACTGAAA	69	Human, Chimp, Dog	537	358
342543	TAACCGCAGTTCTCTGTAGG	60	Human, Chimp, Dog	565	359
342544	TATGTTTAAGTAACCGCAGT	31	Human, Chimp	575	360
342545	AATCACATTTTCATGTTTCA	33	Human, Chimp, Dog	595	361
342546	AACAGACCAATCACATTTTC	27	Human, Mouse, Chimp	603	362
342547	AGAGACCTTGCAGGTGTAAA	33	Human, Chimp, Dog	630	363
342548	GAATTCCTCCAGAGACCTTG	38	Human, Chimp, Dog	640	364
342549	ACACATCATTGAATTCCTCC	49	Human, Chimp, Dog	650	365
342550	GTCACCAGATACACATCATT	21	Human, Chimp, Dog	660	366
342551	CCCATGAGATGGGTCACCAG	76	Human, Mouse, Rat, Chimp	672	367
342552	GTTCAGATCTGCCCCCATGA	73	Human, Chimp	685	368
342553	TTTCACAATGTTGTTCAGAT	45	Human, Chimp, Dog	697	369
342554	GCTTCTGACATTTCACAATG	67	Human, Chimp, Dog	707	370
342555	TCATCTGTAAGCTTCTGACA	68	Human, Chimp	717	371
342556	AGATAAGGAACTGAACATGG	65	Human, Chimp, Dog	737	372
342557	CTTTAGACCTCGGAGAATTT	40	Human, Chimp	760	373
342558	AATGTATATACTTTAGACCT	34	Human, Chimp	770	374
342559	TCCCTGTGAATTATGTCAGC	71	Human, Mouse, Chimp, Dog	792	375
342560	TTAGGTCCCTGTGAATTATG	68	Human, Mouse, Chimp, Dog	797	376
342561	ATTCACAGCTAGATTACTAG	49	Human, Chimp	820	377
342562	TCTGTGTGCCGAGCCAGTCC	66	Human, Chimp	870	378
342563	CATTTCATCATCTGTGTGCC	56	Human, Chimp	880	379
342564	CGTAGCCTGTCATTTCATCA	67	Human, Chimp	890	380
342565	CCACCTAGTGGCCACGTAGC	52	Human, Chimp	904	381
342566	ACAGCTCGGCCATTATGCAT	46	Human, Chimp	992	382
342567	CTTCCAGTCAACAGCTCGGC	72	Human,	1002	383

			Chimp		
342568	AAACAATGTTCTTCCAGTCA	30	Human, Chimp	1012	384
342569	TGGTCTGTACCAGGAAACAA	50	Human, Mouse, Rat, Chimp, Dog	1026	385
342570	CAGACGCATAATCTGCTGAA	68	Human, Chimp	1057	386
342571	GTGTTCCTGTCAGACGCATA	81	Human, Chimp	1067	387
342572	GTTTCTTGCCTCATGGCTTG	16	Human, Mouse, Rat, Chimp	1114	388
342573	ACTGAATATAGTTTCTTGCC	34	Human, Chimp	1124	389
342574	TGAGTCAAAGACTGAATATA	26	Human, Chimp	1134	390
342575	ACATTCGCAAAGTTCATCTT	2	Human, Chimp	1161	391
342576	TTGGCACCAATAAATACATT	50	Human, Mouse, Rat, Chimp, Dog	1176	392
342577	AGTCCAATACAAGCATCTTC	39	Human, Chimp, Dog	1220	393
342578	AGGCATGTGCAAGGGCTTGG	75	Human, Chimp	1262	394
342579	CGTGGTACTGAGCAAAGTAG	60	Human, Mouse, Rat, Chimp	1280	395
342580	TTCATCATCAGGATCGTGGT	73	Human, Chimp	1294	396
342581	CGGCCACTGGTTCATCATCA	66	Human, Chimp	1304	397
342582	GATCATAAGGATCGGCCACT	27	Human, Chimp	1316	398
342583	TCCCTGCTTTCAAAGGACTG	60	Human, Mouse, Rat, Chimp, Dog	1335	399
342584	CTATAAGGAGGTCCCTGCTT	23	Human, Rat, Chimp, Dog	1346	400
342585	TTCCACTCATCTATAAGGAG	58	Human, Chimp	1356	401
342586	GGTCAGGCTTTTCCACTCAT	70	Human, Chimp	1366	402
342587	TCATAGGTCAGGCTTTTCCA	50	Human, Chimp	1371	403
342588	ACTTCATCATAGGTCAGGCT	63	Human, Mouse, Chimp	1377	404
342589	TGATGACTTCATCATAGGTC	53	Human, Mouse, Chimp	1382	405
342590	AAAGCTGATGACTTCATCAT	38	Human, Mouse, Chimp	1387	406
342591	GTGGTGGCACAAAGCTGATG	68	Human, Mouse, Chimp	1397	407
342592	GACTCCATCTCTTCTTGGTC	57	Human, Mouse, Chimp, Dog	1422	408

342593	CCAGGTGCTCAGGACTCCAT	75	Human, Mouse, Chimp	1434	409
342594	AGAAACCAGGTGCTCAGGAC	77	Human, Mouse, Chimp	1439	410
342595	AGAACAGAAACCAGGTGCTC	66	Human, Mouse, Chimp	1444	411
342596	GTGAAGTGGGATCAACAGAA	65	Human, Chimp	1460	412

Antisense compounds having SEQ ID NO: 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, and 412 inhibited p38α RNA expression by at least 10% in this assay.

Compounds having SEQ ID NOs: 347, 348, 350, 351, 353, 354, 355, 356, 357, 358, 359, 367, 368, 370, 371, 372, 375, 376, 378, 379, 380, 381, 383, 385, 386, 387, 392, 394, 395, 396, 397, 399, 401, 402, 403, 404, 405, 407, 408, 409, 410, 411 and 412 inhibited p38α expression by at least 50% in this assay.

Example 21: Dose response experiments- human p38α oligonucleotides

Four of the most active human p38α oligonucleotides (ISIS 186910, 342578, 342651 and 342652) were chosen for dose response studies in human A549 cells at concentrations of 5, 10, 25, 50 and 100 nM. A dose-dependent decrease in p38α mRNA expression was observed with ISIS 342578, 342651 and 342652. For 186910, a dose dependent response was observed from 25 to 100 nM oligonucleotide. A dose dependent decrease in expression of p38α using an antisense oligonucleotide to an unrelated

gene (PP2A) was not observed.

A dose response experiment was also performed in human HepG2 cells with ISIS 100872, 342578, 342651 amd 342652 at the same concentrations as in the A549 cells. Dose-dependent inhibition of mRNA expression was observed for ISIS 342758, 342651 and 342652. For 100872, a dose dependent response was observed from 25 to 100 nM oligonucleotide. A dose dependent decrease in expression of p38α using an antisense oligonucleotide to an unrelated gene (PTP1B) was not observed. In addition, little or no inhibition of p38β mRNA expression was observed in A549 cells with 5, 10, 25, 50 or 100 nM concentrations of these oligonucleotides.

Lastly, p38α protein reduction was also observed 60 hours after transfection of HepG2 and A549 cells In HepG2 cells, the reduction in protein level was about 50% for ISIS 100872, 60% for ISIS 342578, 90% for ISIS 342561 and 87% for ISIS 342652. In A549 cells, ISIS 100872 did not reduce protein levels; however, the reduction in protein level was about 95% for ISIS 342578, 85% for ISIS 342561 and 80% for ISIS 342652. Specific inhibition of p38α expression was observed in HepG2 cells.